

## SEARCH STATISTICS

Scores: Mean Median Standard Deviation  
19 73 42.88

Times: CPU Total Elapsed  
00:01:14.89 00:03:25.00

Number of residues: 1211939  
Number of sequences optimized: 3953

The scores below are sorted by optimized score.  
Significance is calculated based on optimized score.

3 100% identical sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. P80713	Complete sequence of the matu	295	295	295	6.44	0
2. P80504	Sequence encoded by human tis	295	295	295	6.44	0
3. P81503	Human tissue factor	295	295	295	6.44	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
4. P93986	**** 6 standard deviations above mean **** Human tissue factor apoprotei	295	293	293	6.39	0
5. R28067	**** 5 standard deviations above mean **** Sequence encoded by truncated	251	251	251	5.41	0
6. R39392	**** 4 standard deviations above mean **** Truncated tissue factor.	218	217	217	4.62	0
7. R07072	Human tissue factor activator	209	177	207	4.38	0
8. R10065	**** 3 standard deviations above mean **** Newcastle disease virus (NDV)	553	7	157	3.22	0
9. R14480	Newcastle disease virus immun	553	7	156	3.19	0
10. R22217	Sequence of interleukin 5 rec	415	6	155	3.17	0
11. R22211	Sequence of interleukin 5 (IL	415	6	155	3.17	0
12. R22212	Sequence of interleukin 5 (IL	398	6	155	3.17	0
13. P70176	Sequence of Newcastle Disease	553	7	155	3.17	0
14. R08031	Adenyl cyclase from Bordetell	1706	7	154	3.15	0
15. R05041	Filamentous haemagglutinin A.	3647	6	154	3.15	0
16. R12108	N-terminal deleted adenyl cyc	1445	7	154	3.15	0
17. P93357	Sequence of the catalytic dom	1522	7	154	3.15	0
18. P94365	Sequence of part of adenylate	1705	7	154	3.15	0
19. R04716	Amino acid sequence of the 65	572	6	153	3.12	0
20. R04713	Amino acid sequence of the hu	573	8	153	3.12	0
21. P80215	Sequence of Mycobacterium tub	560	6	153	3.12	0
22. R04715	Amino acid sequence of the 65	573	6	153	3.12	0
23. R27481	RP-III residual protease.	806	6	153	3.12	0
24. R27745	Extracellular factor related	1822	6	153	3.12	0
25. P80364	M. leprae 65kD antigen.	588	6	152	3.10	0
26. R06376	Product of the sscI gene.	950	7	152	3.10	0
27. R05701	Human carbastatin polypeptide	673	7	152	3.10	0
28. P70768	Epstein-Barr virus glycoprote	927	7	152	3.10	0
29. P82115	Fibronectin binding protein.	1018	6	152	3.10	0
30. R13251	PECAM-1.	738	7	152	3.10	0
31. R22220	Sequence of secretory interle	396	6	151	3.08	0
32. R10941	Mutant protease (delta137-139	1968	10	151	3.08	0
33. R11137	GAP6 encoded by lambda clone	1047	7	151	3.08	0
34. R13335	HypB protein.	544	6	151	3.08	0
35. R25336	Lambda clone 101 protien.	1047	7	151	3.08	0
36. R33181	L3T4 mutant M8.	454	7	151	3.08	0
37. R12789	M. pneumoniae P1 cytoadhesin p	1627	6	151	3.08	0
38. R06723	Achromobacter protease I.	653	6	151	3.08	0
39. P60723	Sequence of extracellular amy	918	6	151	3.08	0
40. R22219	Sequence of secretory interle	420	6	151	3.08	0

1. FURM-969863-FIG2.PEP (1-295)  
P80713 Complete sequence of the mature and precursor form

ID P80713 standard; peptide; 295 AA.  
AC P80713;  
DT 10-SEP-1990 (first entry)  
DE Complete sequence of the mature and precursor forms of human tissue  
DE factor heavy chain proteins (huTFh and pre-huTFh, respectively)  
KW Human tissue factor heavy chain (huTFh); immunoassays;  
KW precursor human tissue factor heavy chain (pre-huTFh);  
KW human tissue factor detection.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
CT Peptide 1 72

FT Protein 33..33  
 FT Region 33..62  
 FT /note="claimed in claim 26.4"  
 FT Region 58..80  
 FT /note="claimed in claim 26.1"  
 FT Region 62..103  
 FT /note="claimed in claim 22"  
 FT Region 73..81  
 FT /note="claimed in claim 26.6"  
 FT Region 88..103  
 FT /note="claimed in claim 26.7"  
 FT Region 126..155  
 FT /note="claimed in claim 26.9"  
 FT Region 178..199  
 FT /note="claimed in claim 26.2"  
 FT Region 187..199  
 FT /note="claimed in claim 23"  
 FT Region 193..222  
 FT /note="claimed in claim 26.3"  
 FT Region 222..241  
 FT /note="claimed in claim 26.1"  
 PN WD8807543-A.  
 PD 06-OCT-1988.  
 PF 29-MAR-1988; U00998.  
 PR 25-JUN-1987; US-067103.  
 PA (SCRI-) Scripps Clinic Res.  
 PI Eddington TS, Morrissey JH;  
 DR WPI; 88-292837/41.  
 DR N-PSDB; N80743.  
 PT New DNA segment -  
 PT has gene encoding human tissue factor heavy chain protein and is  
 PT useful for inhibiting coagulation  
 PS Disclosure; Fig 1 and Fig 2; 148pp; English.  
 CC It is the amino acid residue sequence of the predominant naturally  
 CC occurring mature protein form residues 33 to 295. The sequence of the  
 CC lesser found mature form begins at amino acid residue number 35 and ends  
 CC at residue 295. A DNA segment which codes for it from about residue 33  
 CC to 295 is claimed in claim 2. Also claimed are antibodies which  
 CC immunoreact with huTFH and the claimed peptides (see FT). The antibodies  
 CC may be used in immunoassays for detection of huTFH. The claimed peptides  
 CC may be used to inhibit the binding of huTF to coagulation factor VII/VIIa  
 CC in vivo. The claimed peptides have an N-terminal H and a C-terminal OH.  
 SQ Sequence 295 AA;  
 SQ 16 A; 12 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;  
 SQ 15 I; 20 L; 20 K; 2 M; 13 F; 14 P; 23 S; 30 T; 7 W; 12 Y; 30 V;

Initial Score = 295 Optimized Score = 295 Significance = 6.44  
 Residue Identity = 100% Matches = 295 Mismatches = 0  
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLGLGVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLGLGVFAQVAGASGTTNTVAAYNLTWKSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLTYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLTYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSHKCRKAGVGQSWKE
      220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X
  
```

2. FURM-969863-FIG2.PEP (1-295)  
 P80504 Sequence encoded by human tissue factor protein (TF)

ID P80504 standard; protein; 295 AA.  
 AC P80504;  
 DT 19-NOV-1990 (first entry)  
 DE Sequence encoded by human tissue factor protein (TF) clone derived from

DE adipose cDNA library  
KW Hybridisation; coagulation; blood clotting; therapy.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..32  
FT Protein 33..295  
PN EP-278776-A.  
PD 17-AUG-1988.  
PF 12-FEB-1988; 301190.  
PR 7-APR-1987; US-035409..  
PR 05-FEB-1988; US-152698.  
PA (GETH) Genentech Inc.  
PI Lawn RM, Wion KL, Vehar GA;  
DR WPI; 88-229602/33.  
DR N-PSDB; n81104.  
PT Tissue factor protein and derivs. -  
PT obtd. by recombinant deoxyribonucleic acid techniques, used to  
PT treat chronic bleeding and coagulation-disorders  
PS Claim 5; Fig 2a-2b; 39pp; English.  
CC Tissue factor protein (TFP) free of substances from its natural source is  
CC claimed. TFP is administered providing a coagulation inducing therapeutic  
CC compsn. for various chronic bleeding disorders. Two oligo probes  
CC representing one possible codon choice for each AA of the N-terminal AA  
CC sequence (60 nucleotides) and internal AA sequence near the C-terminal  
CC (81 nucleotides) were designed and synthesised. cDNA clones of human TFP  
CC were obtd. using the DNA probes first to screen a human placental cDNA  
CC library. 1400 BP EcoRI fragment from a placental clone was used to screen  
CC a human adipose cDNA library. The full length human TFP cDNA was contd.  
CC within the cDNA clone lambda TF14. The full length cDNA was inserted into  
CC an expression plasmid and TFP was expressed using mammalian cells (COS)  
CC cells and E.coli.  
SQ Sequence 295 AA;  
SQ 16 A; 12 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;  
SQ 15 I; 20 L; 20 K; 2 M; 13 F; 14 P; 23 S; 30 T; 7 W; 12 Y; 30 V;

Initial Score = 295 Optimized Score = 295 Significance = 6.44  
Residue Identity = 100% Matches = 295 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEGVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGSWKE
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGSWKE
     220     230     240     250     260     270     280

290   X
NSPLNVS
|||||
NSPLNVS
290   X

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### 3. FURM-969863-FIG2.PEP (1-295) P81503 Human tissue factor

ID P81503 standard; protein; 295 AA.  
AC P81503;  
DT 22-OCT-1990 (first entry)  
DE Human tissue factor  
KW human tissue factor (HTF) apoprotein; procoagulant;  
KW Factor VIII; ss.  
OS synthetic.  
FH Key Location/Qualifiers  
FT Domain 33..220  
FT /label=extracellular domain  
FT Domain 221..243  
FT /label=membrane domain  
FT Domain 244..263  
FT /label=cytoplasmic domain  
FT Peptide 1..32

FT /label=signal peptide  
 PN W08809817-A.  
 PD 15-DEC-1988.  
 PF 08-JUN-1988; U01915.  
 PR 2-JUN-1986; US-062166.  
 PR 14-MAR-1988; US-167870.  
 PA (MOUN-) Mount Sinai Sch Med, (UYVA-) Yale University,  
 PA (UYNY-) City Univ New York, (MOUN) Mount Sinai Hosp Res Fdn.  
 PI Menerson Y, Konigsberg W;  
 DR WPI; 88-368631/51.  
 PT New recombinant cloning vehicle expressing human tissue factor -  
 PT encoding DNA sequences, transformed cells and pure apoprotein  
 PT prods  
 PS Disclosure; pp; English.  
 CC A cloned 2147bp cDNA fragment isolated from human placental cDNA  
 CC library encodes a single chain polypeptide preprotein 295 long.  
 CC The signal sequence is post translationally cleaved to give a mature  
 CC protein of 263 amino acids.  
 CC HTF can be used for inhibiting binding of factor VIII to tissue  
 CC factor.  
 CC See also N81950-2.  
 SQ Sequence 295 AA;  
 SQ 16 A; 12 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;  
 SQ 15 I; 20 L; 20 K; 2 M; 13 F; 14 P; 23 S; 30 T; 7 W; 12 Y; 30 V;

Initial Score = 295 Optimized Score = 295 Significance = 6.44  
 Residue Identity = 100% Matches = 295 Mismatches = 0  
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGGPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGGPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
      220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X

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#### 4. FURM-969863-FIG2.PEP (1-295) P93986 Human tissue factor apoprotein.

ID P93986 standard; protein; 295 AA.  
 AC P93986;  
 DT 22-MAY-1990 (first entry)  
 DE Human tissue factor apoprotein.  
 KW Human tissue factor; coagulation system; anticoagulant; ds.  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Sig\_peptide 1..32  
 FT /label= 32 AA leader  
 FT Domain 33..251  
 FT /label= Extracellular domain  
 FT Domain 252..274  
 FT /label= Membrane domain  
 FT Domain 275..295  
 FT /label= Cytoplasmic domain  
 PN EP-347262-A.  
 PD 20-DEC-1989.  
 PF 19-JUN-1989; 306176.  
 PR 17-JUN-1988; US-208895.  
 PA (UYVA-) Yale Univ, (UYNY-) City Univ New York.  
 PI Menerson Y, Konigsberg W;  
 DR WPI; 89-372479/51.  
 DR N-PSDB; N92782.  
 PT Cloning and expression of human tissue factor - for the prodn. of  
 PT diagnostic reagents, anticoagulant agents and for experimental studies

PS Disclosure; pp; English.  
CC The protein is human tissue factor, which may be cloned from plasmid or  
CC bacteriophage vectors to produce pure or truncated tissue factor, useful  
CC for diagnostic reagents, anticoagulant agents and experimental purposes.  
CC Extracellular domain can be removed and used as a soluble tissue factor  
CC for use as diagnostic reagents, anticoagulant agents and experimental  
CC studies.  
SQ Sequence 295 AA;  
SQ 15 A; 13 R; 16 N; 11 D; 0 B; 5 C; 10 Q; 21 E; 0 Z; 17 G; 1 H;  
SQ 15 I; 20 L; 20 K; 2 M; 13 F; 15 P; 24 S; 29 T; 6 W; 12 Y; 30 V;

Initial Score = 293 Optimized Score = 293 Significance = 6.39  
Residue Identity = 98% Matches = 292 Mismatches = 3  
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARRLLLGVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGSWKE
     220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X
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5. FURM-969863-FIG2.PEP (1-295)  
R28067 Sequence encoded by truncated tissue factor (tTF)

ID R28067 standard; Protein; 251 AA.  
AC R28067;  
DT 02-APR-1993 (first entry)  
DE Sequence encoded by truncated tissue factor (tTF) cDNA.  
KW Activated factor VII; factor VIIa; truncated tissue factor.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Peptide 1..32  
FT /label= leader  
PN W09218870-A.  
PD 29-OCT-1992.  
PF 09-APR-1992; U02898.  
PR 10-APR-1991; US-683682.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
PI Morrissey JJ;  
DR WPI; 92-382277/46.  
DR N-PSDB; Q29716.  
PT Assay for factor VIIa utilising truncated tissue factor - used to  
PT monitor factor VIIa therapy in haemophiliac(s), to screen for  
PT elevated factor VIIa levels and assess risk of thrombosis  
PS Disclosure; Fig 1; 37pp; English.  
CC Starting with clone pCTF543 a TF1-219 deletion mutant was  
CC constructed that contained the coding sequence for the predicted  
CC leader peptide and extracellular domains, but lacked the predicted  
CC transmembrane and cytoplasmic domains. This version of the protein  
CC retains cofactor activity but fails to support conversion of  
CC factor VII to VIIa. The essential difference between truncated  
CC tissue factor and wild-type tissue factor is that truncated tissue  
CC factor is no longer tethered to the phospholipid membrane surface.  
SQ Sequence 251 AA;  
SQ 13 A; 11 R; 14 N; 11 D; 0 B; 4 C; 9 Q; 20 E; 0 Z; 14 G; 0 H;  
SQ 7 I; 16 L; 17 K; 2 M; 11 F; 13 P; 19 S; 30 T; 6 W; 11 Y; 23 V;

Initial Score = 251 Optimized Score = 251 Significance = 5.41  
Residue Identity = 100% Matches = 251 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
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METPAWPRVPRPETAVARTLLLGVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90      100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90      100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     X      260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSHKCRKAGVGQSWKE
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFRE
      220     230     240     250

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290  
NSPLNVS

6. FURM-969863-FIG2.PEP (1-295)  
R39392 Truncated tissue factor.

ID R39392 standard; Protein; 218 AA.  
AC R39392;  
DT 12-JAN-1994 (first entry)  
DE Truncated tissue factor.  
KW Monoclonal antibody; zymogen; rapid; protein isolation; calcium;  
KW presence; fusion protein; affinity chromatography.  
OS Homo sapiens.  
PN W09313211-A.  
PD 08-JUL-1993.  
PF 29-DEC-1992; U11270.  
PR 03-JAN-1992; US-816679.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
PI Esmen CT, Morrissey JH, Rezaie A.  
DR WPI: 93-227327/28.  
DR N-PSDB; Q45779.  
PT Fusion protein allowing rapid isolation of protein from soln. -  
PT comprises desired protein and epitope recognised by monoclonal  
PT antibody HPC-4  
PS Disclosure; Page 24,25; 42pp; English.  
CC The sequence is that encoding truncated tissue factor, the  
CC truncated tissue factor protein lacks the predicted transmembrane  
CC and cytoplasmic domains of tissue factor. The truncated tissue  
CC factor is no longer tethered to the phospholipid membrane surface.  
CC This soluble tissue factor is not a cofactor for precursor factor  
CC VII (FVII).  
SQ Sequence 218 AA;  
SQ 7 A; 8 R; 14 N; 11 D; 0 B; 4 C; 8 Q; 18 E; 0 Z; 12 G; 0 H;  
SQ 7 I; 13 L; 17 K; 1 M; 10 F; 9 P; 18 S; 27 T; 4 W; 11 Y; 19 V;

Initial Score = 217 Optimized Score = 217 Significance = 4.62  
Residue Identity = 100% Matches = 218 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```

      10      20      30     X      40      50      60      70
METPAWPRVPRPETAVARTLLLGVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
      GTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
      X      10      20      30

      80      90      100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      40      50      60      70      80      90      100     110

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      120     130     140     150     160     170     180

      220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSHKCRKAGVGQSWKE
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFRE
      190     200     210     X

```

290  
NSPLNVS

7. FURN-969863-FIG2.PEP (1-295)  
R07072 Human tissue factor activator.

ID R07072 standard; protein; 209 AA.  
AC R07072  
DT 10-JAN-1991 (first entry)  
DE Human tissue factor activator.  
KW Tissue factor; renal disease; sandwich immunoassay.  
OS Homo sapiens.  
PN M09008956-A.  
PD 07-AUG-1990.  
PF 02-FEB-1990; J00127.  
PR 02-FEB-1989; JP-02263.  
PR 17-FEB-1989; JP-036228.  
PR 18-APR-1989; JP-096458.  
PR 04-DEC-1989; JP-314602.  
PA (TEIJ) TEIJIN KK.  
PI Koike Y, Sumi Y, Ichikawa Y;  
DR WPI: 90-261027/34.  
PT Human tissue factor activator detection in human urine - by  
PT sandwich immunoassay, for diagnosis of renal disease  
PS Disclosure; page 5; 54pp; Japanese.  
CC This apoprotein of human tissue factor (thromboplastin) differs  
CC from that of known serum tissue factor. Its presence in e.g.  
CC urine samples is determined using a sandwich immunoassay with one  
CC or more monoclonal antibodies (MAbs) to this sequence. One Ab is  
CC immobilised and the other labelled with e.g. an enzyme. It is  
CC useful in the diagnosis of renal diseases such as nephritis,  
CC nephrosis and kidney stones. See also R07073.  
SQ Sequence 209 AA;  
SQ 7 A; 7 R; 14 N; 11 D; 0 B; 4 C; 7 Q; 15 E; 0 Z; 10 G; 0 H;  
SQ 7 I; 13 L; 16 K; 1 M; 9 F; 9 P; 19 S; 27 T; 4 W; 10 Y; 19 V;

Initial Score = 177 Optimized Score = 207 Significance = 4.38  
Residue Identity = 99% Matches = 209 Mismatches = 0  
Gaps = 1 Conservative Substitutions = 0

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      10      20      30 X      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
      X      10      20      30      40
      SGTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST

      80      90      100      110      120      130      140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      50      60      70      80      90      100      110

      150      160      170      180      190      200      210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTL-YWKSSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTL-YWKSSSSGKKTAKTNTNEFLIDVDKGEN
      120      130      140      150      160      170      180

      220      230      240 X      250      260      270      280
YCFSVQAVIPSRVTNRKSTDSPVECHGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
YCFSVQAVIPSRVTNRKSTDSPVECH
      190      200      X

290
NSPL

```

8. FURN-969863-FIG2.PEP (1-295)  
R10065 Newcastle disease virus (NDV) F gene product.

ID R10065 standard; Protein; 553 AA.  
AC R10065;  
DT 14-MAR-1991 (first entry)  
DE Newcastle disease virus (NDV) F gene product.  
KW Avipoxvirus; fowlpoxvirus; vaccine.  
OS Newcastle disease virus.  
PN EP-404576-A.  
PD 27-DEC-1990.  
PF 21-JUN-1990; 306806.  
PR 22-JUN-1989; JP-160157.  
PA (JAPG) NIPPON ZEON KK.  
PI Yangida N, Saeki S, Okawa S, Khamogawa K, Iritani Y;  
PI Sawaguchi K;  
DR WPI: 91-001591/01.  
DR Q-PSDB; Q10060.  
PT Recombinant avipox virus - contg. CDNA coding for Newcastle  
PT disease virus in region non-essential for proliferation, used as  
PT live vaccine in fowls

CC VII (FVII).  
 SQ Sequence 672 BP; 221 A; 137 C; 161 G; 153 T;

Initial Score = 644 Optimized Score = 658 Significance = 35.87  
 Residue Identity = 97% Matches = 662 Mismatches = 9  
 Gaps = 5 Conservative Substitutions = 0

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150      160      170      180      190      X 200      210
TCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGG
                                |||||
                                CCGGGACCACTAATACTGTGG
                                X      10      20

220      230      240      250      260      270      280
CAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCAATC
CAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCAATC
      30      40      50      60      70      80      90

290      300      310      320      330      340      350      360
AAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAG
AAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAG
      100      110      120      130      140      150      160

370      380      390      400      410      420      430
AGTGTGACCTCACCAGCAGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCGG
AGTGTGACCTCACCAGCAGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCGG
      170      180      190      200      210      220      230

440      450      460      470      480      490      500
CAGGGAATGTGGAGAGCACCAGTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTACC
CAGGGAATGTGGAGAGCACCAGTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTACC
      240      250      260      270      280      290      300      310

510      520      530      540      550      560      570
TGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAG
TGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAG
      320      330      340      350      360      370      380

580      590      600      610      620      630      640
AAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAA
AAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAA
      390      400      410      420      430      440      450

650      660      670      680      690      700      710      720
TTTATACACTTTATTATTGGAATCTTCAAGTTTCAAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTT
TTTATACACTTTATTATTGGAATCTTCAAGTTTCAAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTT
      460      470      480      490      500      510      520

730      740      750      760      770      780      790
TGATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAAGTGTCAAGCAGTGATTCCCTCCCGAACAGTTAACC
TGATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAAGTGTCAAGCAGTGATTCCCTCCCGAACAGTTAACC
      530      540      550      560      570      580      590

800      810      820      830      840      850      860
GGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACA-TC
GGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAG-AAATA-ACTGCAGTC
      600      610      620      630      640      650      660

870      880      890      900      910      920
ATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTATCATCCTGGCTATATCTCT
--TAGA
670 X

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# 7. FURM-969863-FIG2.SEQ (1-987)

043701 Sequence of the human COL1A1 gene extending from i

ID 043701 standard; DNA; 5931 BP.  
 AC 043701;  
 DT 24-SEP-1993 (first entry)  
 DE Sequence of the human COL1A1 gene extending from intron 25 to exon  
 DE 52.  
 KW Type 1 procollagen; COL1A1; COL2A1; osteoporosis; ss.  
 OS Homo sapiens.  
 PN W09311149-A.  
 PD 10-JUN-1993.  
 PF 01-DEC-1992; U10355.  
 PR 07-DEC-1991; M5-807428



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170      180      190      200      210      220      230
310      320      330      340      350      360      370
TCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGACCTCAC
TCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGACCTCAC
240      250      260      270      280      290      300

380      390      400      410      420      430      440
CGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCCTACCCGGCAGGGAATGTGGA
CGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCCTACCCGGCAGGGAATGTGGA
310      320      330      340      350      360      370      380

450      460      470      480      490      500      510
GAGCACCGGTTCTGCTGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCT
GAGCACCGGTTCTGCTGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCT
390      400      410      420      430      440      450

520      530      540      550      560      570      580      590
CGGACAGCCAACAATTTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGAC
CGGACAGCCAACAATTTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGAC
460      470      480      490      500      510      520

600      610      620      630      640      650      660
TTTAGTCAGAAAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAATTTATACACTTTA
TTTAGTCAGAAAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAATTTATACACTTTA
530      540      550      560      570      580      590

670      680      690      700      710      720      730
TTATTGGAATCTTCAAGTTCAGGAAAGAAACAGCCAAAACAAACACTAATGAGTTTTTGATTGATGTGGA
TTATTGGAATCTTCAAGTTCAGGAAAGAAACAGCCAAAACAAACACTAATGAGTTTTTGATTGATGTGGA
600      610      620      630      640      650      660

740      750      760      770      780      790      800
TAAAGGAGAAACTACTGTTTCAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGA
TAAAGGAGAAACTACTGTTTCAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGA
670      680      690      700      710      720      730      740

810      820      830      840      850      860      870
CAGCCCGGTAGAGTGATGAGGCCAGGAGAAAGGGGAATTAGAGAAATATTCTACATCATTGGAGCTGTGGT
CAGCCCGGTAGAGTGATGAGGCCAGGAGAAAGGGGAATTAGAGAAATATTCTACATCATTGGAGCTGTGGT
750      760      770      780      790      X

880      890      900      910
ATTGTGGTCATCATCCTTGTATCATCCTGGC

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6. FURM-969863-FIG2.SEQ (1-987)  
045779 Truncated tissue factor gene.

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ID   Q45779 standard; cDNA; 672 BP.
AC   Q45779;
DT   12-JAN-1994 (first entry)
DE   Truncated tissue factor gene.
KW   Monoclonal antibody; zymogen; rapid; protein isolation; calcium;
KW   presence; fusion protein; affinity chromatography; tTF; ss.
OS   Homo sapiens.
FH   Key                     Location/Qualifiers
FT   CDS                     4..660
FT   /*tag= a
FT   misc_recomb              1..6
FT   /*tag= b
FT   misc_recomb              67..72
FT   /*tag= c
PN   W09313211-A.
PD   08-JUL-1993.
PF   29-DEC-1992; U11270.
PR   03-JAN-1992; US-816679.
PA   (OKLA-) OKLAHOMA MED RES FOUND.
PI   Esmon CT, Morrissey JH, Rezaie A.
DR   WPI; 93-227327/28.
DR   P-PSDB; R39392.
PT   Fusion protein allowing rapid isolation of protein from soln. -
PT   comprises desired protein and epitope recognised by monoclonal
PT   antibody HPC-4
PS   Example 1; Page 24,25; 42pp; English.
CC   The sequence is that encoding truncated tissue factor, the
CC   truncated tissue factor protein lacks the predicted transmembrane
CC   and cytoplasmic domains of tissue factor. The truncated tissue
CC   factor is no longer tethered to the phospholipid membrane surface.
CC   This soluble tissue factor is not a cofactor for precursor factor

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ACTAATGAGTTTTGATTGATGGATAAAGGAGAAAAGCTACTGTTTCAGTGTTCAGGAGTGAATTCCTCC  
730 740 750 760 770 780 790

790 800 810 820 830 840 850  
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA  
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA  
800 810 820 830 840 850 860

860 870 880 890 900 910 920  
ATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTGCATCATCTGGCTATATCTCTACAC  
ATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTGCATCATCTGGCTATATCTCTACAC  
870 880 890 900 910 920 930

930 940 950 960 970 980 X  
AAGTGTAGAAAGGAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA  
AAGTGTAGAAAGGAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCAC  
940 950 960 970 980 990 1000

TGTTGGAGCTACTGCAAATGCTATATTGCACTGTGACCGAG  
1010 1020 1030 1040

5. FURM-969863-FIG2.SEQ (1-987)  
Q29716 Sequence of truncated tissue factor (tTF) cDNA.

ID Q29716 standard; cDNA; 795 BP.  
AC Q29716;  
DT 02-APR-1993 (first entry)  
DE Sequence of truncated tissue factor (tTF) cDNA.  
KW Activated factor VII; factor VIIa; truncated tissue factor; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT sig\_peptide 1..33  
FT /\*tag= a  
FT CDS 34..130  
FT /\*tag= b  
FT /product= leader peptide  
PN WD9218870-A.  
PD 29-OCT-1992.  
PF 09-APR-1992; U02898.  
PR 10-APR-1991; US-683682.  
PA (OKLA-) OKLAHOMA MED RES FOUND.  
PI Morrissey JJ;  
DR WPI; 92-382277/46.  
DR P-PSDB; R28067.  
PT Assay for factor VIIa utilising truncated tissue factor - used to  
PT monitor factor VIIa therapy in haemophiliac(s), to screen for  
PT elevated factor VIIa levels and assess risk of thrombosis  
PS Disclosure; Fig 1; 37pp; English.  
CC Starting with clone pCTF543 a TF1-219 deletion mutant was  
CC constructed that contained the coding sequence for the predicted  
CC leader peptide and extracellular domains, but lacked the predicted  
CC transmembrane and cytoplasmic domains. This version of the protein  
CC retains cofactor activity but fails to support conversion of  
CC factor VII to VIIa. The essential difference between truncated  
CC tissue factor and wild-type tissue factor is that truncated tissue  
CC factor is no longer tethered to the phospholipid membrane surface.  
SQ Sequence 795 BP; 234 A; 186 C; 199 G; 176 T;

Initial Score = 781 Optimized Score = 785 Significance = 43.73  
Residue Identity = 98% Matches = 786 Mismatches = 9  
Gaps = 2 Conservative Substitutions = 0

20 30 40 50 60 X 70 80  
GGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCGG  
CG--TTCCGCTCGATCTCGCGG  
X 10 20

90 100 110 120 130 140 150  
CCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCCGTCGCTCGGACGCT  
CCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCCGTCGCTCGGACGCT  
30 40 50 60 70 80 90

160 170 180 190 200 210 220 230  
CCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTT  
CCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTT  
100 110 120 130 140 150 160

240 250 260 270 280 290 300  
AACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCAACCCGTCATCAAGTCTACACTGT  
AACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCAACCCGTCATCAAGTCTACACTGT  
AACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCAACCCGTCATCAAGTCTACACTGT

FT Sig\_peptide 112..207  
FT /\*tag= a  
FT Mat\_peptide 208..999  
FT /\*tag= c  
PN EP-347262-A.  
PD 20-DEC-1989.  
PF 19-JUN-1989; 306176.  
PR 17-JUN-1988; US-208895.  
PA (UYVA-) Yale Univ, (UYNY-) City Univ New York.  
PI Nemerson Y, Konigsberg W;  
DR WPI; 89-372479/51.  
DR P-PSDB; P93986.  
PT Cloning and expression of human tissue factor - for the prodn. of  
PT diagnostic reagents, anticoagulant agents and for experimental studies.  
PS Disclosure; pp; English.  
CC cDNA fragment codes for the entire human tissue factor gene, which may  
CC be cloned into plasmid or bacteriophage vectors to produce pure or  
CC truncated tissue factor, useful for diagnostic reagents, anticoagulant  
CC agents and experimental purposes.  
SQ Sequence 2147 BP; 613 A; 455 C; 477 G; 602 T;

Initial Score = 983 Optimized Score = 983 Significance = 55.32  
Residue Identity = 99% Matches = 983 Mismatches = 4  
Gaps = 0 Conservative Substitutions = 0

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      X      10      20      30      40      50      60
      CTGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
CGGGCGAACCCCTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC
      10 X      20      30      40      50      60      70
      70      80      90      100     110     120     130
GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
      80      90      100     110     120     130     140
      140     150     160     170     180     190     200
CCCGAGACCGCGCTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
CCCGAGACCGCGCTCGCTCGGAGGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
      150     160     170     180     190     200     210
      210     220     230     240     250     260     270
ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCC
ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCC
      220     230     240     250     260     270     280
      280     290     300     310     320     330     340
AAACCCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAATGCTTTTAC
AAACCCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAATGCTTTTAC
      290     300     310     320     330     340     350     360
350     360     370     380     390     400     410     420
ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
      370     380     390     400     410     420     430
      430     440     450     460     470     480     490
TTCTCTACCCGGCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAG
TTCTCTACCCGGCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAG
      440     450     460     470     480     490     500
      500     510     520     530     540     550     560
TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTAGAGTTTTGAACAGGTGGGAACAAAAGTG
TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTAGAGTTTTGAACAGGTGGGAACAAAAGTG
      510     520     530     540     550     560     570
      570     580     590     600     610     620     630
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
      580     590     600     610     620     630     640
      640     650     660     670     680     690     700
GGCAAGGACTTAATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAAC
GGCAAGGACTTAATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAAC
      650     660     670     680     690     700     710     720
710     720     730     740     750     760     770     780
ACTAATGAGTTTTTATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAAGCAGTGATTCCTCC

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80      90      100     110     120     130     140
150      160      170      180      190      200      210
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
150      160      170      180      190      200      210

220      230      240      250      260      270      280
GCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
GCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
220      230      240      250      260      270      280

290      300      310      320      330      340      350      360
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACA
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACA
290      300      310      320      330      340      350      360

370      380      390      400      410      420      430
GAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCG
GAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCTACCCG
370      380      390      400      410      420      430

440      450      460      470      480      490      500
GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTAC
GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTAC
440      450      460      470      480      490      500

510      520      530      540      550      560      570
CTGGAGACAAACCTCGGACAGCCAAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA
CTGGAGACAAACCTCGGACAGCCAAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA
510      520      530      540      550      560      570

580      590      600      610      620      630      640
GAAGATGAACGGACTTTAGTCAGAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA
GAAGATGAACGGACTTTAGTCAGAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA
580      590      600      610      620      630      640

650      660      670      680      690      700      710      720
ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT
ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT
650      660      670      680      690      700      710      720

730      740      750      760      770      780      790
TTGATTGATGTGGATAAAGGAGAAAACACTGTTTCAGTGTTCAAGCAGTGATTCCCTCCCGAACAGTTAAC
TTGATTGATGTGGATAAAGGAGAAAACACTGTTTCAGTGTTCAAGCAGTGATTCCCTCCCGAACAGTTAAC
730      740      750      760      770      780      790

800      810      820      830      840      850      860
CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC
CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC
800      810      820      830      840      850      860

870      880      890      900      910      920      930
ATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAG
ATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAG
870      880      890      900      910      920      930

940      950      960      970      980      X
GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCACTGTTGGAGCTAC
940      950      960      970      980      990      1000

TGCAATGCTATATTGCACTGTGACCGAG
1010      1020      1030

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4. FURM-969863-FIG2.SEQ (1-987)  
N92782 cDNA of entire human tissue factor apoprotein.

ID N92782 standard; cDNA; 2147 BP.  
AC N92782;  
DT 22-MAY-1990 (first entry)  
DE cDNA of entire human tissue factor apoprotein.  
KW Human tissue factor; coagulation system; anticoagulant; ds.  
OS Homo sapiens.  
CU

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GGCAAGGACTTAATTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAAC
650      660      670      680      690      700      710      720
710      720      730      740      750      760      770      780
ACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAAAGTACTGTTTCAGTGTTCAGCAGTGATTCCCTCC
ACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAAAGTACTGTTTCAGTGTTCAGCAGTGATTCCCTCC
730      740      750      760      770      780      790
790      800      810      820      830      840      850
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
CGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
800      810      820      830      840      850      860
860      870      880      890      900      910      920
ATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTCTATCTCTCTACAC
ATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTCTATCTCTCTACAC
870      880      890      900      910      920      930
930      940      950      960      970      980      X
AAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA
AAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCAC
940      950      960      970      980      990      1000
TGTGGAGCTACTGCAATGCTATATTGCACTGTGACCGAG
1010      1020      1030      1040

```

### 3. FURM-969863-FIG2.SEQ (1-987)

N81104 Sequence of human tissue factor protein (TFP) clone

```

ID   N81104 standard; DNA; 2127 BP.
AC   N81104;
DT   19-NOV-1990 (first entry)
DE   Sequence of human tissue factor protein (TFP) clone derived from
DE   adipose cDNA library
KW   Hybridisation; coagulation; blood clotting; therapy; ds.
OS   Homo sapiens.
FH   Key          Location/Qualifiers
FT   sig_peptide  100..195
FT   /*tag= a
FT   mat_peptide  196..987
FT   /*tag= b
PN   EP-278776-A.
PD   17-AUG-1988.
PF   12-FEB-1988; 301190.
PR   7-APR-1987; US-035409.
PR   05-FEB-1988; US-152698.
PA   (GETH) Genentech Inc.
PI   Lawn RM, Wion KL, Vehar GA;
DR   WPI; 88-229602/33.
DR   P-PSDB; P80504.
PT   Tissue factor protein and derivs. -
PT   obtd. by recombinant deoxyribonucleic acid techniques, used to
PT   treat chronic bleeding and coagulation-disorders
PS   Claim 4; Fig 2a-2b; 39pp; English.
CC   Tissue factor protein (TFP) free of substances from its natural source is
CC   claimed. TFP administered to provide a coagulation inducing therapeutic
CC   compsn. for various chronic bleeding disorders. Two oligo probes
CC   representing one possible codon choice for each AA of the N-terminal AA
CC   sequence (60 nucleotides) and internal AA sequence near the C-terminal
CC   (81 nucleotides) were designed and synthesised. cDNA clones of human TFP
CC   were obtd. using the DNA probes first to screen a human placental cDNA
CC   library. 1400 BP EcoRI fragment from a placental clone was used to screen
CC   a human adipose cDNA library. The full length human TFP cDNA was contd.
CC   within the cDNA clone lambda TF14. The full length cDNA was inserted into
CC   an expression plasmid and TFP was expressed using mammalian cells (COS)
CC   cells and E.coli.
SQ   Sequence 2127 BP; 606 A; 450 C; 472 G; 599 T;

```

```

Initial Score = 987 Optimized Score = 987 Significance = 55.55
Residue Identity = 100% Matches = 987 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

```

```

X      10      20      30      40      50      60      70
CTCGCACTCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
|||||
CTCGCACTCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
X      10      20      30      40      50      60      70

```

```

      80      90     100     110     120     130     140
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC

```

FT /\*tag= a  
FT /product=human tissue factor  
FT sig\_peptide 112..207  
FT /\*tag= b  
FT mat\_peptide 208..996  
FT /\*tag= c  
FT /product=apoprotein  
PN W08809817-A.  
PD 15-DEC-1988.  
PF 08-JUN-1988; U01915.  
PR 2-JUN-1986; US-062166.  
PR 14-MAR-1988; US-167870.  
PA (MDUN-) Mount Sinai Sch Med, (UYVA-) Yale University,  
PA (UYNY-) City Univ New York, (MDUN) Mount Sinai Hosp Res Fdn.  
PI Menerson Y, Konigsberg W;  
DR WPI; 88-368631/51.  
PT New recombinant cloning vehicle expressing human tissue factor -  
PT encoding DNA sequences, transformed cells and pure apoprotein  
PT prods  
PS Disclosure; pp; English.  
CC The fragment encodes a single chain polypeptide preprotein 295  
CC long. The signal sequence is post translationally cleaved to give  
CC a mature protein of 263 amino acids.  
CC HTF can be used for inhibiting binding of factor VIII to tissue  
CC factor.  
CC See also N81950-2.  
SQ Sequence 2147 BP; 613 A; 454 C; 477 G; 603 T;

Initial Score = 987 Optimized Score = 987 Significance = 55.55  
Residue Identity = 100% Matches = 987 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```

      X      10      20      30      40      50      60
      CTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCAGCCCCACGGGC
CGGGCGAACCCCTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCAGCCCCACGGGC
10 X      20      30      40      50      60      70
      70      80      90      100     110     120     130
      GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
      GCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGC
      80      90      100     110     120     130     140
      140     150     160     170     180     190     200
      CCGGAGACCGCGTGCCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
      CCGGAGACCGCGTGCCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT
      150     160     170     180     190     200     210
      210     220     230     240     250     260     270
      ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCC
      ACAAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAACCC
      220     230     240     250     260     270     280
      280     290     300     310     320     330     340
      AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC
      AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC
      290     300     310     320     330     340     350     360
      350     360     370     380     390     400     410     420
      ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
      ACAACAGACACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTC
      370     380     390     400     410     420     430
      430     440     450     460     470     480     490
      TTCTCTACCCGGCAGGGAATGTGGAGAGACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAG
      TTCTCTACCCGGCAGGGAATGTGGAGAGACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCAGAG
      440     450     460     470     480     490     500
      500     510     520     530     540     550     560
      TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTG
      TTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTG
      510     520     530     540     550     560     570
      570     580     590     600     610     620     630
      AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
      AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT
      580     590     600     610     620     630     640
      640     650     660     670     680     690     700
      GCGAAGCACTTAATTTATACACTTTATTATTGAAATCTTCAAGTTCAGGAAACAAAACACCCAAAACAAAC
```

```

170      180      190      200      210      220      230
GCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACTTGA
GCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACTTGA
230      240      250      260      270      280      290

240      250      260      270      280      290      300      310
AATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTAATCAAGTCTACACTGTTCAAATAA
AATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTAATCAAGTCTACACTGTTCAAATAA
300      310      320      330      340      350      360      370

320      330      340      350      360      370      380
GCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAGAGTGTGACCTCACCGACGAGA
GCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACAGAGTGTGACCTCACCGACGAGA
380      390      400      410      420      430      440

390      400      410      420      430      440      450
TTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGAGCACCG
TTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGAGCACCG
450      460      470      480      490      500      510

460      470      480      490      500      510      520
GTTCTGCTGGGGAGCCTCTGTATGAGAAGTCCCCAGAGTTCACACCTTACCTGGAGACAAACCTCGGACAGC
GTTCTGCTGGGGAGCCTCTGTATGAGAAGTCCCCAGAGTTCACACCTTACCTGGAGACAAACCTCGGACAGC
520      530      540      550      560      570      580

530      540      550      560      570      580      590
CAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCA
CAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCA
590      600      610      620      630      640      650

600      610      620      630      640      650      660      670
GAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGA
GAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGA
660      670      680      690      700      710      720      730

680      690      700      710      720      730      740
AATCTTCAAGTTCAGGAAGAAAACAGCCAAAACAACTAATGAGTTTTTGATTGATGTGGATAAAGGAG
AATCTTCAAGTTCAGGAAGAAAACAGCCAAAACAACTAATGAGTTTTTGATTGATGTGGATAAAGGAG
740      750      760      770      780      790      800

750      760      770      780      790      800      810
AAACTACTGTTTCAAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGG
AAACTACTGTTTCAAGTGTTCAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGG
810      820      830      840      850      860      870

820      830      840      850      860      870      880
TAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGG
TAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGG
880      890      900      910      920      930      940

890      900      910      920      930      940      950
TCATCATCCTTGTATCATCCTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGA
TCATCATCCTTGTATCATCCTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGA
950      960      970      980      990      1000      1010

960      970      980      X
AGGAGAACTCCCCACTGAATGTTTCATAA
AGGAGAACTCCCCACTGAATGTTTCATAAAGGAAGCACTGTTGAGCTACTGCAAATGCTATATTGCACTGT
1020      1030      1040      1050      1060      1070      1080      1090
GACCGAG

```

2. FURM-969863-FIG2.SEQ (1-987)  
N81953 Encodes human tissue factor

ID N81953 standard; cDNA; 2147 BP.  
AC N81953;  
DT 22-OCT-1990 (first entry)  
DE Encodes human tissue factor  
KW human tissue factor (HTF) apoprotein; procoagulant;  
KW Factor VIII; ss.  
OS synthetic.  
FH Key Location/Qualifiers  
ET cns 112 999

11. Q20269	Gene encoding AE-III (peptidy	3383	114	427	5.45	0
12. Q25107	DHFR-APP fusion protein (pBBK	4670	112	416	5.34	0
13. Q22995	Sequence encoding 53 kD cellu	1182	110	420	5.22	0
14. Q11563	Encodes E-cadherin from dog k	4333	110	432	5.22	0
15. Q39967	PKC-alpha cDNA.	3305	107	432	5.05	0
16. N40141	Sequence of human factor IX g	11866	107	402	5.05	0
17. N40176	Sequence of human factor IX g	11873	107	401	5.05	0
*** 4 standard deviations above mean ***						
18. N60202	Interferon-pseudo-omega-2.	2132	105	420	4.94	0
19. Q13802	Non-receptor linked protein t	2287	105	385	4.94	0
20. Q03661	Maize C3 sequence encoding ac	2546	105	421	4.94	0
21. Q10543	BamHI J-I fragment carrying s	2721	104	395	4.88	0
22. Q10212	BamHI J-I fragment carrying s	2721	104	395	4.88	0
23. N50525	Bacillus thuringiensis var. i	3756	104	422	4.88	0
24. Q32366	MAGE-10 genomic DNA.	920	102	259	4.76	0
25. N81341	Recombinant plasmid pMP1 cont	4133	102	409	4.76	0
26. N71017	Sequence of LAV/HTLV III gag	5340	102	431	4.76	0
27. N60142	Sequence of ARV-2 cloned in p	2467	101	324	4.71	0
28. Q31938	p41 gag gene (fusion of p25 g	2467	100	323	4.65	0
29. Q13673	SUP-B27 t(1;19) translocation	2837	99	422	4.59	0
30. Q13675	E2A/pr1 fusion transcript fro	2922	99	421	4.59	0
31. Q49757	pTK gene HpTK5.	3969	99	409	4.59	0
32. Q45503	Sequence encoding an antibody	1657	98	356	4.53	0
33. Q24174	M13IX421.	7294	98	415	4.53	0
34. Q24172	M13IX30.	7445	98	414	4.53	0
35. Q14752	HIV-1(MN-ST1) env protein-enc	9746	98	428	4.53	0
36. Q12528	Thymidylate phosphohydrolase.	1611	97	354	4.48	0
37. Q27487	PT42 promoter and 5' gene por	2370	97	382	4.48	0
38. Q24171	M13IX22.	7320	97	411	4.48	0
39. Q33150	CAT-LacZ alpha-peptide trans-	623	96	243	4.42	0
40. Q27243	CAT-LacZ alpha-peptide trans-	623	96	243	4.42	0

1. FURM-969863-FIG2.SEQ (1-987)  
Q20349 Thromboplastin clone 2b-Apr5.

ID Q20349 standard; cDNA; 2189 BP.  
AC Q20349;  
DT 09-APR-1992 (first entry)  
DE Thromboplastin clone 2b-Apr5.  
KW Thromboplastin; Ig; fusion protein; ss.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT CDS 160..1044  
FT /\*tag= a  
FT /label= thromboplastin  
PN EP-464533-A.  
PD 08-JAN-1992.  
PF 24-JUN-1991; 110368.  
PR 28-JUN-1990; DE-020607.  
PA (BEHW) BEHRINGWERKE AG.  
PA (GEHO-) GENERAL HOSPITAL CORP.  
PI Laufer L, Oquendo P, Zettlmeiss G, Seed B;  
DR WPI; 92-009794/02.  
PT Soluble fusion protein useful in treatment or diagnosis - contg.  
PT immunoglobulin constant region and e.g. thromboplastin, cytokine  
PT or receptor, expressed in mammalian cells  
PS Disclosure; Fig 2; 21pp; German.  
CC Based on the thromboplastin DNA sequence published by Scarpati et al.,  
CC Biochemistry, Bd. 26 (1987), 5234-5238, two oligonucleotide probes  
CC are derived (Q20350-51). A human placenta cDNA bank is screened.  
CC Several clones are obtained and clone 2b-Apr5 is isolated. The derived  
CC amino acid sequence is as described by Scarpati et al.  
CC See also Q20349-57.  
SQ Sequence 2189 BP; 617 A; 470 C; 487 G; 615 T;

Initial Score = 987 Optimized Score = 987 Significance = 55.55  
Residue Identity = 100% Matches = 987 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```

                                X      10      20
                                CTGCACTCCCTCTGGCCGGCC
GAGGTCGACGGTATCGATAAGCTTGATATCGAATTCTCTCGGCGAACCCCTCGCACTCCCTCTGGCCGGCC
      20      30      40      50      60      70      80

      30      40      50      60      70      80      90
CAGGGGCGCCTTCAGCCCAACCTCCCGAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGG
CAGGGGCGCCTTCAGCCCAACCTCCCGAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGG
      90     100     110     120     130     140     150

     100     110     120     130     140     150     160
TAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGCTCGCTCGGACGCTCCTGCTCG
TAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGCTCGCTCGGACGCTCCTGCTCG
     160     170     180     190     200     210     220

```



#authors Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.  
 #journal Mol. Cell. Biol. (1989) 9:2567-2573  
 #title A growth factor-responsive gene of murine BALB/c 3T3 cells  
 encodes a protein homologous to human tissue factor.  
 #cross-references MUID:89343974  
 #accession A32318  
 ##molecule\_type mRNA  
 ##residues 1-294 ##label HAR  
 ##cross-references GB:M26071  
 REFERENCE A39046  
 #authors Ranganathan, G.; Blatti, S.P.; Subramanian, M.; Fass, D.N.;  
 Maihle, N.J.; Getz, M.J.  
 #journal J. Biol. Chem. (1991) 266:496-501  
 #title Cloning of murine tissue factor and regulation of gene  
 expression by transforming growth factor type beta1.  
 #cross-references MUID:91093171  
 #accession A39046  
 ##molecule\_type mRNA  
 ##residues 1-25, 'I', 27-294 ##label RAN  
 ##cross-references GB:J05713  
 ##note 26-Thr was also found  
 COMMENT Tissue factor is an integral membrane glycoprotein that serves as a  
 receptor for plasma coagulation factor VIIa. The complex  
 initiates the extrinsic coagulation pathway.  
 COMMENT Expression of tissue factor can be induced in a variety of tissues  
 by certain growth factors and inflammatory stimuli.  
 CLASSIFICATION #superfamily tissue factor  
 KEYWORDS blood coagulation; glycoprotein; membrane protein  
 FEATURE  
 1-29 #domain signal sequence #status predicted #label SIG  
 30-294 #protein tissue factor #status predicted #label MAT  
 30-251 #domain extracellular #status predicted #label EXT  
 252-274 #domain transmembrane #status predicted #label TM  
 75-83,218-241 #disulfide bonds #status predicted  
 37,57,169,200 #binding\_site carbohydrate (Asn) (covalent) #status  
 predicted  
 275 #binding\_site fatty acid (Cys) (covalent) #status  
 experimental  
 SUMMARY #length 294 #molecular-weight 32923 #checksum 9197  
 SEQUENCE

Initial Score = 87 Optimized Score = 219 Significance = 5.50  
 Residue Identity = 52% Matches = 158 Mismatches = 114  
 Gaps = 13 Conservative Substitutions = 16

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKVSTNFKTILEWEPKPVNQVYTVQIST
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
MAILVRPRL---AALAPT-FLGCLLLQVTAGAGIPEK--AFNLTWISTDFKTILEWQPKPTNYTYTVQISD
X      10      20      30      40      50      60

      80      90     100     110     120     130
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYP-AGNVESTGS-----AGEPLYENSPEFTPYLET
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
RSRNWKNKCFSTTDTTECDLTDEIVKDVWYAEAKVLSVPRNSVHGDGDQLVIHGEEPPFTNAPKFLPYRDT
70      80      90     100     110     120     130

140     150     160     170     180     190     200     210
NLGQPTIQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYLYWKSSSSGKKTAKTNTNEFLID
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
NLGQPVIIQFEQDGRKLVVVKDSLTLVRKNGFTLRLQVFGKDLGYIITRKGSSTGKKTNTITNEFSID
140     150     160     170     180     190     200     210

220     230     240     250     260     270     280
VDKGENYCFVSQAVIPSRVTNRKSTDSPVECMGQEGEFREIFYIIGAVVFVVIILVILAIHLKCRKAGV
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
VEEGVSYCFVQAMIFSRKTQNSPGSSTVCTEQWKSFLGETLIIVGAVVLLATIFIILSLCKRRKNRA
220     230     240     250     260     270     280

290 X
GQSMKENSPLNVS
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GQKGG-NTPSRLA
290 X
  
```

# 8. FURM-969863-FIG2.PEP (1-295) VGNZU1 fusion glycoprotein - Newcastle disease virus (str

ENTRY VGNZU1 #type complete  
 TITLE fusion glycoprotein - Newcastle disease virus (strain Ulster)  
 ORGANISM #formal name Newcastle disease virus  
 DATE 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change  
 30-Jun-1993  
 ACCESSIONS A29823  
 REFERENCE A92799  
 #authors Millar, N.S.; Chambers, P.; Emerson, P.T.  
 #journal J. Gen. Virol. (1989) 70:117-120

```

IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
150      160      170      180      190      200      210
YCFSVQAVIPSRRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAI SLHKCRKAGVGQSWKE
220      230      240      250      260      270      280
YCFSVQAVIPSRKRKRQSPESLTCTSRQGRAREMFFIIGAVV-VVALLIIVLSVTVYKCRKARACPSGKE
220      230      240      250      260      270      280
290      X
NSPLNVS
||||:
SSPLNIA
290      X

```

# 6. FURM-969863-FIG2.PEP (1-295)

S23681 tissue factor - rabbit

```

ENTRY      S23681      #type complete
TITLE      tissue factor - rabbit
ORGANISM    #formal name Oryctolagus cuniculus #common_name domestic
              rabbit
DATE        22-Nov-1993; #sequence_revision 22-Nov-1993; #text_change
              22-Nov-1993
ACCESSIONS  S23681
REFERENCE   S23681
#authors    Pawashe, A.; Ezekowitz, M.; Lin, T.C.; Horton, R.; Bach, R.;
              Konigsberg, W.
#journal     Thromb. Haemost. (1991) 66:315-320
#title       Molecular cloning, characterization and expression of cDNA
              for rabbit brain tissue factor.
#cross-references MUID:92081032
#accession    S23681
##status      preliminary
##residues     1-260 ##label PAW
##cross-references EMBL:X53521
SUMMARY      #length 260 #molecular-weight 29312 #checksum 2601
SEQUENCE

```

```

Initial Score = 209 Optimized Score = 229 Significance = 5.88
Residue Identity = 71% Matches = 186 Mismatches = 56
Gaps = 1 Conservative Substitutions = 18

```

```

10      20      30      X      40      50      60      70
METPAWPRVPRPETAVARILLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEKPVNQVYTVQIST
              |
              ADTTGRAYNLTKWSTNFKTILEWEKPSIDHVVYTVQIST
              X      10      20      30
80      90      100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
:
RLENWKSCKFLTAETECDLTDEVVKDVGQTYMARVLSYPARNGNTTGFPEEPPFRNSPEFTPYLDTNLGQPT
40      50      60      70      80      90      100     110
150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
120     130     140     150     160     170     180
220     230     240     250     260     270     280
YCFSVQAVIPSRRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAI SLHKCRKAGVGQSWKE
YCFSVQAVIPSRKRKRQSPESLTCTSRQGRAREMFFIIGAVV-VVALLIIVLSVTVYKCRKARACPSGKE
190     200     210     220     230     240     250

```

```

290      X
NSPLNVS
||||:
SSPLNIA
260

```

# 7. FURM-969863-FIG2.PEP (1-295)

KFMS3 tissue factor precursor - mouse

```

ENTRY      KFMS3      #type complete
TITLE      tissue factor precursor - mouse
ALTERNATE_NAMES coagulation factor III
ORGANISM    #formal name Mus musculus #common_name house mouse
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
              30-Sep-1993
ACCESSIONS  A32318; A39046
REFERENCE   A32318

```



Residue Identity = 100% Matches = 295 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNRNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNRNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280

290  X
NSPLNVS
|||||
NSPLNVS
290  X
```

4. FURM-969863-FIG2.PEP (1-295)

KFB03 tissue factor precursor - bovine

```
ENTRY      KFB03      #type complete
TITLE      tissue factor precursor - bovine
ALTERNATE_NAMES coagulation factor III
ORGANISM    #formal name Bos primigenius taurus #common name cattle
DATE        30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change
            30-Sep-1993
ACCESSIONS  J01319
REFERENCE   J01319
#authors    Takayenoki, Y.; Muta, T.; Miyata, T.; Iwanaga, S.
#journal     Biochem. Biophys. Res. Commun. (1991) 181:1145-1150
#title       cDNA and amino acid sequences of bovine tissue factor.
#cross-references MUID:92109720
#contents    Adrenal gland
#accession   J01319
            ##molecule_type mRNA
            ##residues      1-292 ##label TAK
            ##cross-references GB:S74147
            ##note          part of this sequence, including the amino end of the
                           mature protein, was confirmed by protein sequencing
COMMENT      Tissue factor is an integral membrane glycoprotein that serves as a
            receptor for plasma coagulation factor VIIa. The complex
            initiates the extrinsic coagulation pathway.
COMMENT      Expression of tissue factor can be induced in a variety of tissues
            by certain growth factors and inflammatory stimuli.
CLASSIFICATION #superfamily tissue factor
KEYWORDS      blood coagulation; glycoprotein; membrane protein
FEATURE
1-35          #domain signal sequence #label SIG
36-292        #protein tissue factor #status experimental #label MAT
36-248        #domain extracellular #status predicted #label EXT
249-271       #domain transmembrane #status predicted #label TMM
272-292       #domain intracellular #status predicted #label INT
81-89,215-238 #disulfide bonds #status predicted
43,153,181    #binding site carbohydrate (Asn) (covalent) #status
            predicted
118,124       #binding site carbohydrate (Thr) (covalent) #status
            predicted
274          #binding site fatty acid (Cys) (covalent) #status
            experimental
SUMMARY      #length 292 #molecular-weight 32475 #checksum 1836
SEQUENCE
```

Initial Score = 148 Optimized Score = 257 Significance = 6.92  
Residue Identity = 69% Matches = 204 Mismatches = 71  
Gaps = 3 Conservative Substitutions = 17

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGHVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
MATPNGPRVPCPQAARALLFGLVLIQAGVAGTTDVVVAYNITWKSTNFKTILEWEPKPINHVYTVQISP
Y      10      20      30      40      50      60      70
```

290 X  
 NSPLNVS  
 |||||  
 NSPLNVS  
 290 X

### 3. FURM-969863-FIG2.PEP (1-295)

KFHU3 tissue factor precursor - human

ENTRY KFHU3 #type complete  
 TITLE tissue factor precursor - human  
 ALTERNATE\_NAMES coagulation factor III  
 ORGANISM #formal name Homo sapiens #common name man  
 DATE 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change  
 03-Feb-1994  
 ACCESSIONS A28320; A29062; A29672; A29008  
 REFERENCE A74171  
 #authors Spicer, E.K.; Horton, R.; Bloem, L.; Bach, R.; Williams,  
 K.R.; Guha, A.; Kraus, J.; Lin, T.C.; Nemerson, Y.;  
 Konigsberg, W.H.  
 #journal Proc. Natl. Acad. Sci. U.S.A. (1987) 84:5148-5152  
 #title Isolation of cDNA clones coding for human tissue factor:  
 primary structure of the protein and cDNA.  
 #cross-references MUID:87260946  
 #accession A28320  
 ##molecule\_type mRNA  
 ##residues 1-295 ##label SPI  
 ##cross-references GB:J02931  
 REFERENCE A29062  
 #authors Morrissey, J.H.; Fakhrai, H.; Edgington, T.S.  
 #journal Cell (1987) 50:129-135  
 #title Molecular cloning of the cDNA for tissue factor, the cellular  
 receptor for the initiation of the coagulation protease  
 cascade.  
 #cross-references MUID:87244317  
 #accession A29062  
 ##molecule\_type mRNA  
 ##residues 1-295 ##label MOR  
 ##cross-references GB:J02931  
 ##note part of this sequence, including the amino end of the  
 mature protein, was confirmed by protein sequencing  
 REFERENCE A29672  
 #authors Scarpati, E.M.; Wen, D.; Broze Jr., G.J.; Miletich, J.P.;  
 Flandermeyer, R.R.; Siegel, N.R.; Sadler, J.E.  
 #journal Biochemistry (1987) 26:5234-5238  
 #title Human tissue factor: cDNA sequence and chromosome  
 localization of the gene.  
 #cross-references MUID:88050796  
 #accession A29672  
 ##molecule\_type mRNA  
 ##residues 1-259, 'A', 261-295 ##label SCA  
 ##cross-references GB:M16553  
 REFERENCE A37422  
 #authors Bach, R.; Konigsberg, W.H.; Nemerson, Y.  
 #journal Biochemistry (1988) 27:4227-4231  
 #title Human tissue factor contains thioester-linked palmitate and  
 stearate on the cytoplasmic half-cystine.  
 #contents annotation; disulfide bonds and fatty acid binding site  
 COMMENT Tissue factor is an integral membrane glycoprotein that serves as a  
 receptor for plasma coagulation factor VIIa. The complex  
 initiates the extrinsic coagulation pathway.  
 COMMENT Expression of tissue factor can be induced in a variety of tissues  
 by certain growth factors and inflammatory stimuli.  
 GENETICS  
 #gene GDB:F3  
 #map position 1p22-p21  
 CLASSIFICATION #superfamily tissue factor  
 KEYWORDS blood coagulation; glycoprotein; lipoprotein; membrane  
 protein  
 FEATURE  
 1-32 #domain signal sequence #status experimental #label SIG  
 33-295 #protein tissue factor #status experimental #label MAT  
 33-251 #domain extracellular #status predicted #label EXT  
 252-274 #domain transmembrane #status predicted #label TMM  
 275-295 #domain intracellular #status predicted #label INT  
 81-89,218-241 #disulfide bonds #status experimental  
 43 #binding\_site carbohydrate (Asn) (covalent) #status  
 experimental  
 156,169 #binding\_site carbohydrate (Asn) (covalent) #status  
 predicted  
 277 #binding\_site fatty acid (Cys) (covalent) #status  
 experimental  
 SUMMARY #length 295 #molecular-weight 33067 #checksum 4014  
 SEQUENCE

Initial Score = 295 Normalized Score = 295 Significance = 8.33

SUMMARY #length 295 #molecular-weight 33067 #checksum 4014  
SEQUENCE

Initial Score = 295 Optimized Score = 295 Significance = 8.33  
Residue Identity = 100% Matches = 295 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETN LGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETN LGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVIIAISLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVIIAISLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280

290 X
NSPLNVS
|||||
NSPLNVS
290 X
```

2. FURM-969863-FIG2.PEP (1-295)

A43645 tissue factor - human

ENTRY A43645 #type complete  
TITLE tissue factor - human  
ORGANISM #formal name Homo sapiens #common name man  
DATE 03-Mar-1993 #sequence\_revision 03-Mar-1993 #text\_change 30-Sep-1993  
ACCESSIONS A43645  
REFERENCE A43645  
#authors Mackman, N.; Morrissey, J.H.; Fowler, B.; Edgington, T.S.  
#journal Biochemistry (1989) 28:1755-1762  
#title Complete sequence of the human tissue factor gene, a highly regulated cellular receptor that initiates the coagulation protease cascade.  
#accession A43645  
##status preliminary  
##molecule\_type DNA  
##residues 1-295 ##label MAC  
##cross-references GB:J02844; GB:J02846  
SUMMARY #length 295 #molecular-weight 33067 #checksum 4014  
SEQUENCE

Initial Score = 295 Optimized Score = 295 Significance = 8.33  
Residue Identity = 100% Matches = 295 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

```
X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLL GWVFAQVAGASGTTNTVAAYNLTKSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETN LGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETN LGQPT
      80      90     100     110     120     130     140

     150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
     150     160     170     180     190     200     210

     220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVIIAISLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVIIAISLHKCRKAGVGQSWKE
     220     230     240     250     260     270     280
```

Scores:                    Mean                    Median                    Standard Deviation  
                                  71                    126                    26.89

Times:                    CPU                    Total Elapsed  
                                  00:01:53.98                    00:05:47.00

Number of residues:                    1682879  
 Number of sequences optimized:                    4259

The scores below are sorted by optimized score.  
 Significance is calculated based on optimized score.

3 100% identical sequences to the query sequence were found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. A47574	tissue factor precursor - hum	295	295	295	8.33	0
2. A43645	tissue factor - human	295	295	295	8.33	0
3. KFHU3	tissue factor precursor - hum	295	295	295	8.33	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
4. KFB03	**** 6 standard deviations above mean **** tissue factor precursor - bov	292	148	257	6.92	0
5. KFRB3	tissue factor precursor - rab	292	209	254	6.80	0
6. S23681	**** 5 standard deviations above mean **** tissue factor - rabbit	260	209	229	5.88	0
7. KFMS3	tissue factor precursor - mou	294	87	219	5.50	0
8. VGNZU1	**** 3 standard deviations above mean **** fusion glycoprotein - Newcastle	553	7	157	3.20	0
9. A46329	fusion glycoprotein precursor	553	7	157	3.20	0
10. B46329	fusion glycoprotein precursor	553	7	157	3.20	0
11. C46329	fusion glycoprotein precursor	553	7	157	3.20	0
12. VGBEX1	glycoprotein X precursor - eq	797	8	156	3.16	0
13. A36830	fusion glycoprotein precursor	553	7	156	3.16	0
14. D46329	fusion glycoprotein precursor	553	7	156	3.16	0
15. VGNZTE	fusion glycoprotein precursor	553	7	156	3.16	0
16. H46329	fusion glycoprotein precursor	553	7	156	3.16	0
17. S07422	fusion glycoprotein precursor	553	7	156	3.16	0
18. F46329	fusion glycoprotein precursor	553	7	155	3.12	0
19. VGNZGB	fusion glycoprotein - Newcastle	553	7	155	3.12	0
20. A30588	140K adhesin protein - Mycopl	1444	7	155	3.12	0
21. J80090	attachment protein MgPa - Myc	1444	7	155	3.12	0
22. VGNZNV	fusion glycoprotein - Newcastle	553	7	155	3.12	0
23. S06345	fusion glycoprotein precursor	553	7	155	3.12	0
24. E46329	fusion glycoprotein precursor	553	7	155	3.12	0
25. G46329	fusion glycoprotein precursor	553	7	155	3.12	0
26. B36830	fusion glycoprotein precursor	553	7	155	3.12	0
27. VGNZND	fusion glycoprotein - Newcastle	553	7	155	3.12	0
28. I46329	fusion glycoprotein precursor	553	7	155	3.12	0
29. XDEC	asparaginase (EC 3.5.1.1) II	348	6	154	3.09	0
30. A42632	apCAM=cell adhesion molecule	932	13	154	3.09	0
31. OYBRC	cyclolysin - Bordetella pertu	1706	7	154	3.09	0
32. A32800	mitochondrial protein P1 prec	573	8	153	3.05	0
33. A34173	mitochondrial protein P1 prec	573	9	153	3.05	0
34. A41931	heat shock protein hsp60, hsp	573	9	153	3.05	0
35. HHMS60	heat shock protein 60 precurs	573	9	153	3.05	0
36. A29646	invasin - Yersinia pseudotube	986	7	153	3.05	0
37. S13089	heat shock protein 60 precurs	573	9	153	3.05	0
38. QRMSP1	microtubule-associated protei	2464	7	152	3.01	0
39. S18449	variant surface glycoprotein	514	8	152	3.01	0
40. S20548	leptomycin B resistance prote	1362	7	152	3.01	0

1. FURM-969863-FIG2.PEP (1-295)

A47574 tissue factor precursor - human

```
ENTRY      A47574      #type complete
TITLE      tissue factor precursor - human
ORGANISM   #formal name Homo sapiens #common name man
DATE       31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change
           31-Dec-1993
ACCESSIONS A47574
REFERENCE  A47574
           #authors    Fisher, K.L.; Gorman, C.M.; Vehar, G.A.; O'Brien, D.P.; Lawn,
           R.M.
           #journal     Thromb. Res. (1987) 48:89-99
           #title       Cloning and expression of human tissue factor cDNA.
           #accession   A47574
           ##status     preliminary
           ##molecule_type mRNA
           ##residues    1-295 ##label FIS
           ##cross-references GR:M27474
```

Times: CPU Total Elapsed  
00:01:33.96 00:03:13.00

Number of residues: 1520603  
Number of sequences optimized: 3760

The scores below are sorted by optimized score.  
Significance is calculated based on optimized score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
1. TF_HUMAN	TISSUE FACTOR PRECURSOR (TF)	295	295	295	61.80	0

The list of other best scores is:

Sequence Name	Description	Length	Init. Score	Opt. Score	Sig.	Frame
2. TF_BOVIN	TISSUE FACTOR PRECURSOR (TF)	292	148	257	46.15	0
3. TF_RABIT	TISSUE FACTOR PRECURSOR (TF)	292	209	254	44.91	0
4. TF_MOUSE	TISSUE FACTOR PRECURSOR (TF)	294	87	219	30.49	0
5. VGLF_NDVQ	FUSION GLYCOPROTEIN PRECURSOR	553	7	157	4.94	0
6. VGLF_NDVU	FUSION GLYCOPROTEIN PRECURSOR	553	7	157	4.94	0
7. BRAZ_PSEAE	BRANCHED CHAIN AMINO ACID TRA	437	6	156	4.53	0
8. VGLF_NDVH4	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
9. VGLF_NDVA	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
10. VGLF_NDVT	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
11. VGLF_NDVH3	FUSION GLYCOPROTEIN PRECURSOR	553	7	156	4.53	0
12. VGLX_HSVVB	GLYCOPROTEIN X PRECURSOR.	797	8	156	4.53	0
13. ADP1_MYCGE	140 KD ADHESIN PRECURSOR (ATT	1444	7	155	4.12	0
14. OCT1_HUMAN	OCTAMER-BINDING TRANSCRIPTION	743	7	155	4.12	0
15. VGLF_NDVB	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
16. VGLF_NDVTG	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
17. VGLF_NDVM	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
18. VGLF_NDVL	FUSION GLYCOPROTEIN PRECURSOR	553	7	155	4.12	0
19. VGLF_NDVI	FUSION GLYCOPROTEIN PRECURSOR	553	7	154	3.71	0
20. CYAA_BORPE	CALMODULIN-SENSITIVE ADENYLAT	1706	7	154	3.71	0
21. ASG2_ECOLI	L-ASPARAGINASE II PRECURSOR (	348	6	154	3.71	0
22. I230_MOUSE	INDOLEAMINE 2,3-DIOXYGENASE (	407	6	153	3.30	0
23. P60_HUMAN	MITOCHONDRIAL MATRIX PROTEIN	573	8	153	3.30	0
24. P60_RAT	MITOCHONDRIAL MATRIX PROTEIN	573	9	153	3.30	0
25. P60_CRIGR	MITOCHONDRIAL MATRIX PROTEIN	573	9	153	3.30	0
26. A4_DROME	BETA-AMYLOID-LIKE PROTEIN PRE	886	7	153	3.30	0
27. P60_MOUSE	MITOCHONDRIAL MATRIX PROTEIN	573	9	153	3.30	0
28. INVX_VERPS	INVASIN.	985	7	153	3.30	0
29. ATC1_YEAST	CALCIUM-TRANSPORTING ATPASE 1	950	7	152	2.88	0
30. FTSZ_BACSU	CELL DIVISION FTSZ PROTEIN.	382	7	152	2.88	0
31. SYFB_BACSU	PHENYLALANYL-TRNA SYNTHETASE	804	7	152	2.88	0
32. MAPB_MOUSE	MICROTUBULE-ASSOCIATED PROTEI	2464	7	152	2.88	0
33. PEC1_HUMAN	PLATELET ENDOTHELIAL CELL ADH	738	7	152	2.88	0
34. AROA_KLEPN	3-PHOSPHOSHIKIMATE 1-CARBOXYV	427	6	152	2.88	0
35. VS14_TRYBB	VARIANT SURFACE GLYCOPROTEIN	514	8	152	2.88	0
36. CH60_BACSU	60 KD CHAPERONIN (PROTEIN CPN	544	7	151	2.47	0
37. CH60_THEP3	60 KD CHAPERONIN (HEAT SHOCK	538	7	151	2.47	0
38. MOT1_YEAST	PROBABLE HELICASE MOT1.	1867	8	151	2.47	0
39. FLIF_BACSU	FLAGELLAR M-RING PROTEIN (FLA	536	7	151	2.47	0
40. ICEN_PSESY	ICE NUCLEATION PROTEIN.	1200	8	151	2.47	0

1. FURM-969863-FIG2.PEP (1-295)  
TF\_HUMAN TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF HUMAN STANDARD; PRT; 295 AA.  
AC P13726;  
DT 01-JAN-1990 (REL. 13, CREATED)  
DT 01-JAN-1990 (REL. 13, LAST SEQUENCE UPDATE)  
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
GN F3.  
OS HOMO SAPIENS (HUMAN).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; PRIMATES.  
RN [1]  
RP SEQUENCE FROM N.A.  
RM 89247359  
RA MACKMAN N. MORRISSEY J. H. FOWLER B. EDINGTON T. S.:



RL BIOCHEMISTRY 28:1755-1762(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RM 87260946  
 RA SPICER E.K., HORTON R., BLOEM L., BACH R., WILLIAMS K.R., GUHA A.,  
 RA KRAUS J., LIN T.C., NEMERSON Y., KONIGSBERG W.H.;  
 RL PROC. NATL. ACAD. SCI. U.S.A. 84:5148-5152(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RM 87244317  
 RA MORRISSEY J.H., FAKHRAI H., EDGINGTON T.S.;  
 RL CELL 50:129-135(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RM 88050796  
 RA SCARPATI E.M., WEN D., BROZE G.J. JR., MILETICH J.P.,  
 RA FLANDERMEYER R.R., SIEGEL N.R., SADLER J.E.;  
 RL BIOCHEMISTRY 26:5234-5238(1987).  
 RN [5]  
 RP DISULFIDE BONDS, AND PALMITOYLATION.  
 RM 89000604  
 RA BACH R., KONIGSBERG W.H., NEMERSON Y.;  
 RL BIOCHEMISTRY 27:4227-4231(1988).  
 CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES  
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROLYSIS. TF PLAYS A ROLE IN  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -!- INDUCTION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF  
 CC CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1  
 CC AND TNF, AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND  
 CC VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE  
 CC RESPONSE.  
 DR EMBL; J02931; HSTFP.  
 DR EMBL; M16553; HSTF1.  
 DR EMBL; J02846; HSTFPB.  
 DR PIR; A28320; KFHU3.  
 DR PIR; A43645; A43645.  
 DR MIM; 134390; TENTH EDITION.  
 DR PROSITE; PS00621; TISSUE FACTOR.  
 KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.  
 FT SIGNAL 1 32  
 FT CHAIN 33 295 TISSUE FACTOR.  
 FT DOMAIN 33 251 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 252 274 POTENTIAL.  
 FT DOMAIN 275 295 CYTOPLASMIC (POTENTIAL).  
 FT SITE 46 48 WKS MOTIF.  
 FT SITE 77 79 WKS MOTIF.  
 FT SITE 190 192 WKS MOTIF.  
 FT CARBOHYD 156 156 POTENTIAL.  
 FT CARBOHYD 169 169 POTENTIAL.  
 FT DISULFID 81 89  
 FT DISULFID 218 241  
 FT LIPID 277 277 PALMITATE.  
 FT CONFLICT 260 260 V -> A (IN REF. 4).  
 SQ SEQUENCE 295 AA; 33067 MW; 494480 CN;

Initial Score = 295 Optimized Score = 295 Significance = 61.80  
 Residue Identity = 100% Matches = 295 Mismatches = 0  
 Gaps = 0 Conservative Substitutions = 0

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|||||
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
|||||
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
|||||
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
|||||
YCFSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGVGQSWKE
      220     230     240     250     260     270     280

```

|||||  
NSPLNVS  
290 X

2. FURM-969863-FIG2.PEP (1-295)

TF\_BOVIN TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF BOVIN STANDARD; PRT: 292 AA.  
AC P30931;  
DT 01-JUL-1993 (REL. 26, CREATED)  
DT 01-JUL-1993 (REL. 26, LAST SEQUENCE UPDATE)  
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
OS BOS TAURUS (BOVINE).  
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
OC EUTHERIA; ARTIODACTYLA.  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
RC TISSUE=ADRENAL GLAND;  
RM 92109720  
RA TAKAYENOKI Y., MUTA T., MIYATA T., IWANAGA S.;  
RL BIOCHEM. BIOPHYS. RES. COMMUN. 181:1145-1150(1991).  
CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES  
CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN  
CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
DR EMBL: S74147; S74147.  
DR PIR: J01319; KFB03.  
KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.  
FT SIGNAL 1 35  
FT CHAIN 36 292 TISSUE FACTOR.  
FT DOMAIN 36 248 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 249 271 POTENTIAL.  
FT DOMAIN 272 292 CYTOPLASMIC (POTENTIAL).  
FT SITE 46 48 WKS MOTIF.  
FT CARBOHYD 43 43 POTENTIAL.  
FT CARBOHYD 153 153 POTENTIAL.  
FT CARBOHYD 181 181 POTENTIAL.  
FT DISULFID 81 89 BY SIMILARITY.  
FT DISULFID 215 238 BY SIMILARITY.  
FT LIPID 274 274 PALMITATE (BY SIMILARITY).  
SQ SEQUENCE 292 AA; 32475 MW; 478152 CN;

Initial Score = 148 Optimized Score = 257 Significance = 46.15  
Residue Identity = 69% Matches = 204 Mismatches = 71  
Gaps = 3 Conservative Substitutions = 17

X 10 20 30 40 50 60 70  
METPAWPRVPRPETAVARTLLGLWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST  
|||  
MATPNCPRVPCPAAVARALLFGLVLIGAGVAGTTDVVAYNITWKSTNFKTILEWEPKPINHVYTVQISP  
X 10 20 30 40 50 60 70  
  
80 90 100 110 120 130 140  
KSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVSTGSAGEPLYENSPEFTPYLETNLGQPT  
: |||  
RLGNWKNKCFYTTNTECDVTDEIVKNVRETYLARVLSYPA---DTSSSTVEPPFTNSPEFTPYLETNLGQPT  
80 90 100 110 120 130 140  
  
150 160 170 180 190 200 210  
IQSFEQVGTKNVTVEDERTLVRNNTFLSLRDVFGKDLIYTLVYWKSSSGKKTAKTNTNEFLIDVDKGEN  
|||  
IQSFEQVGTKNVTVQDARTLVRANSFLSLRDVFGKDLNYTLVYWKASSTGKKKATTNTNGFLIDVDKGEN  
150 160 170 180 190 200 210  
  
220 230 240 250 260 270 280  
YCFSVQAVIPSRTVNRKSTDSPECMGQEGEFREIFYIIGAVVFVVIILVILAIHLKCRKAGVGQSWKE  
|||  
YCFHVQAVILSRVRNGKSPESPIKTSHEKVLSTELFFIIGTVMLVIIIFIVVLSVSLHKCRKVRAERSGKE  
220 230 240 250 260 270 280

290 X  
NSPLNVS  
|||||  
NTPLNAA  
290 X

3. FURM-969863-FIG2.PEP (1-295)

TF\_RABIT TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF RABIT STANDARD; PRT: 292 AA.  
AC P24055;  
DT 01-MAR-1992 (REL. 21, CREATED)  
DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)

DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
 OS DRYCTOLAGUS CUNICULUS (RABBIT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; LAGOMORPHA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=HEART;  
 RM 91200676  
 RA ANDREWS B.S., REHMENTULLA A., FOWLER B.J., EDGINGTON T.S., MACKMAN N.;  
 RL GENE 98:265-269(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RM 92081032  
 RA PAWASHE A., EZEKOWITZ M., LIN T.C., HORTON R., BACH R., KONIGSBERG W.;  
 RL THROMB. HAEMOST. 66:315-320(1991).  
 CC --!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES  
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC --!- TISSUE SPECIFICITY: BRAIN, HEART.  
 CC --!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 DR EMBL; M55390; OCRF.  
 DR PIR; JU0441; KFRB3.  
 DR PROSITE; P500621; TISSUE FACTOR.  
 KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.  
 FT SIGNAL 1 32  
 FT CHAIN 33 292 TISSUE FACTOR.  
 FT DOMAIN 33 250 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 250 271 POTENTIAL.  
 FT DOMAIN 272 292 CYTOPLASMIC (POTENTIAL).  
 FT SITE 44 46 WKS MOTIF.  
 FT SITE 75 77 WKS MOTIF.  
 FT CARBOHYD 41 41 POTENTIAL.  
 FT CARBOHYD 114 114 POTENTIAL.  
 FT CARBOHYD 154 154 POTENTIAL.  
 FT CARBOHYD 167 167 POTENTIAL.  
 FT CARBOHYD 182 182 POTENTIAL.  
 FT DISULFID 79 87 BY SIMILARITY.  
 FT DISULFID 216 239 BY SIMILARITY.  
 FT LIPID 274 274 PALMITATE (BY SIMILARITY).  
 SQ SEQUENCE 292 AA; 32738 MW; 459706 CN;

Initial Score = 209 Optimized Score = 254 Significance = 44.91  
 Residue Identity = 69% Matches = 206 Mismatches = 67  
 Gaps = 3 Conservative Substitutions = 19

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLGLWVFAQVAGASGTNTNTVAAYNLTKWSTNFKTILEWEKPVNQVYTVQIST
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
MAPPTRLQVPRPGTAVPYTVLLGLWLLAQVARAADTTGR--AYNLTKWSTNFKTILEWEKPSIDHVVYTVQIST
X      10      20      30      40      50      60      70

      80      90     100     110     120     130     140
KSGDWKSKCFYTTDTECDLTDEIVKDVQKTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNGLGPT
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RLENWKSKCFLTAETECDLTDEVVKDVGGTYMARVLSYPARNGNTTGFPPEPPFRNSPEFTPYLDTNGLGPT
      80      90     100     110     120     130     140

      150     160     170     180     190     200     210
IQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTYLWYKSSSGKKTAKTNTNEFLIDVDKGEN
IQSFEQVGTKLVNTVQDARTLVRNNGTFLSLRAVFGKDLNYTYLWYRASSTGKKTATTNTNEFLIDVDKGEN
      150     160     170     180     190     200     210

      220     230     240     250     260     270     280
YCFSVQAVIPSRITVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAI SLHKCRKAGVGQSWKE
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
YCFSVQAVIPSRKRKQSPESLTETSREOGRAREMFFIIGAVV-VVALLIIVLSVTVYKCRKARAGPSGKE
      220     230     240     250     260     270     280

290 X
NSPLNVS
||||:
SSPLNIA
290 X
  
```

#### 4. FURM-969863-FIG2.PEP (1-295) TF\_MOUSE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR I

ID TF\_MOUSE STANDARD; PRT; 294 AA.  
 AC P20352;  
 DT 01-FEB-1991 (REL. 17, CREATED)  
 DT 01-AUG-1991 (REL. 19, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)

GN CF-3.  
 OS MUS MUSCULUS (MOUSE).  
 DC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 DC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RM 91093171  
 RA RANGANATHAN G., BLATTI S.P., SUBRAMANIAM M., FASS D.N., MAIHLE N.J.,  
 RA GETZ M.J.;  
 RL J. BIOL. CHEM. 266:496-501(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RM 89343974  
 RA HARTZELL S., RYDER K., LANAHAN A., LAU L.F., NATHANS D.;  
 RL MOL. CELL. BIOL. 9:2567-2573(1989).  
 CC -!- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES  
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTOLYSIS. TF PLAYS A ROLE IN  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 DR EMBL; M57896; MMTFA.  
 DR EMBL; M26071; MMTF.  
 DR PIR; A32318; KFM53.  
 DR PROSITE; PS00621; TISSUE FACTOR.  
 KW GLYCOPROTEIN; BLOOD COAGULATION; TRANSMEMBRANE; SIGNAL; LIPOPROTEIN.  
 FT SIGNAL 1 28  
 FT CHAIN 29 294 TISSUE FACTOR.  
 FT DOMAIN 29 251 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 252 274 POTENTIAL.  
 FT DOMAIN 275 294 CYTOPLASMIC (POTENTIAL).  
 FT SITE 245 247 WKS MOTIF.  
 FT CARBOHYD 37 37 POTENTIAL.  
 FT CARBOHYD 57 57 POTENTIAL.  
 FT CARBOHYD 169 169 POTENTIAL.  
 FT CARBOHYD 200 200 POTENTIAL.  
 FT DISULFID 75 83 BY SIMILARITY.  
 FT DISULFID 218 241 BY SIMILARITY.  
 FT LIPID 275 275 PALMITATE (BY SIMILARITY).  
 FT CONFLICT 26 26 I -> T (IN REF. 2).  
 SQ SEQUENCE 294 AA; 32935 MW; 468130 CN;

Initial Score = 87 Optimized Score = 219 Significance = 30.49  
 Residue Identity = 52% Matches = 158 Mismatches = 114  
 Gaps = 13 Conservative Substitutions = 16

```

X      10      20      30      40      50      60      70
METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNLTKWSTNFKTILEWEPKPVNQVYTVQIST
|      |      |      |      |      |      |      |      |      |      |      |
MAILVRPRL---AALAPT-FLGCLLLQVIAGAGIPEK--AFNLTWISTDFKTILEWQPKPTNYTYTVQISD
X      10      20      30      40      50      60

      80      90     100     110     120     130
KSGDWKSKCFYTTDTECDLTDEIVKDVKQTYLARVFSYP-AGNVESTGS-----AGEPLYENSPEFTPYLET
|      |      |      |      |      |      |      |      |      |      |      |
RSRNWKNKCFSTTDTTECDLTDEIVKDVTHWAYEAKVLSVPRRNSVHGDGDLVIHGEEPPFTNAPKFLPYRDT
70      80      90     100     110     120     130

140     150     160     170     180     190     200     210
NLGQPTIQSFEQVGTKVNVTVEDERTLVRNNTFLSLRDVFGKDLIYTYWKSSSSGKKTAKTNTNEFLID
|      |      |      |      |      |      |      |      |      |      |      |
NLGQPVIIQFEQDGRKLNVVVKDSLTLVRKNGFTLTLRQVFGKDLGYIITYRKGSSTGKKTNIITNNEFSID
140     150     160     170     180     190     200     210

      220     230     240     250     260     270     280
VDKGENYCFVSQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHKCRKAGV
|      |      |      |      |      |      |      |      |      |      |      |
VEEGVSYCFVQAMIFSRKTQNSPGSSTVCTEQWKSFLGETLIIVGAVVLLATIFIILLSISLCKRRKNRA
220     230     240     250     260     270     280

      290 X
GQSWKENSPLNVS
|      |
GQKGGK-NTPSRLA
290 X
  
```

5. FURM-969863-FIG2.PEP (1-295)  
 VGLF\_NDVQ FUSION GLYCOPROTEIN PRECURSOR (CONTAINS: FUSION GL  
 ID VGLF\_NDVQ STANDARD; PRT: 553 AA.  
 AC P33615;  
 DT 01-FEB-1994 (REL. 28, CREATED)  
 DT 01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)  
 DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)  
 DE FUSION GLYCOPROTEIN PRECURSOR (CONTAINS: FUSION GLYCOPROTEINS F1 AND  
 RE

```

XX
FH Key Location/Qualifiers
FH
FT sig_peptide 64..144
FT source 1..1683
FT /strain="Sprague-Dawley"
FT /organism="Rattus norvegicus"
FT /cell_type="aortic smooth muscle"
FT CDS 64..951
FT /note="NCBI gi: 464011"
FT /product="tissue factor protein"
FT /codon_start=1
XX
SQ Sequence 1683 BP; 473 A; 379 C; 379 G; 452 T; 0 other;

```

```

Initial Score = 321 Optimized Score = 555 Significance = 21.64
Residue Identity = 60% Matches = 600 Mismatches = 321
Gaps = 69 Conservative Substitutions = 0

```

```

      10      20      30      40      50      60      70
CTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
      |      |      |      |      |      |      |
      X      10      20      30
      80      90      100     110     120     130     140
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCC-CCGAGACCGC
      |      |      |      |      |      |      |
      40      50      60      70      80      90
CCGGACCTCGCCAGCAGCCCTTGACATGGCTATCCC-CATG---CG---CCCGCGCTCCTAG-CGGC
      |      |      |      |      |      |      |
      100     110     120     130     140     150     160
CGTCGCTCGGACGCTCCTGCTCGGTGGTCTTCGCC--CAGGTGGCCGGCGCTTCAGGCA---CTACAAAT
      |      |      |      |      |      |      |
      170     180     190     200     210     220     230
AAAG-CGTTTAACTTGAATATCACTGATTCAAGACAATCTTGGAGTGGCAACCGAAACCCACCAA
      |      |      |      |      |      |      |
      240     250     260     270     280     290     300
GTCATCAAGTCTACACTGTTCAAATA-AGCACTA-AGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAA
      |      |      |      |      |      |      |
      310     320     330     340     350
CTATACCTACACTGTTTCAATAAGCGATAGATCTAGAAACTGGA-AATACAAATGCA---CTGGAACCACA
      |      |      |      |      |      |      |
      360     370     380     390     400
CAGACACAGAGTG---TGACCTACCGA---CGA-GATTGTGAA--GGA--TGTAAGCA---GACGTA-CT
      |      |      |      |      |      |      |
      410     420     430     440     450     460     470
-TGGCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGA-GCACCGGTTCTGCTGGGGAG---CCTCTGTA
      |      |      |      |      |      |      |
      480     490     500     510     520     530     540
TGAGAACTCCCAG-AGTTCACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTGAAC
      |      |      |      |      |      |      |
      550     560     570     580     590     600     610
AGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCCTAA
      |      |      |      |      |      |      |
      620     630     640     650     660     670     680     690
GCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGA
      |      |      |      |      |      |      |      |
      700     710     720     730     740     750     760
AAACAGCCAAACAAACACTAATGAGTTTTGATTGATGTGGATAAAGGAGAAAAGTACTGTTTCAGTGTTC
      |      |      |      |      |      |      |
      770     780     790     800     810     820     830
AAGCAGTGATTCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTA-TGGGCCAGGAG

```

```

GTCCCATGGAGGAAC-CAAC---TCATGGAAAGGAAACACTCTTTGGAACATCATGGGAGGAACCGCCAT-
380      390      400      410      420      430      440

480      490      500      510      520      530      540
TGAGAACTCCCCAG-AGTTACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTGAGATTTTGAAC
TTACAAATGCCCGGAAGTTTTTACCTTACCGAGATACAAAAATTGGACAGCCAGTAATTGAGAAGTATGAAC
450      460      470      480      490      500      510

550      560      570      580      590      600      610
AGGTGGGAACAAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAA
AAGGCGGTACGAAACTGAAGGTGACTGTAAAAGACTCATTACATTAGTCAGAAAGAATGGTACATTCTCA
520      530      540      550      560      570      580

620      630      640      650      660      670      680      690
GCCTCCGGGATGTTTTTGGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGA
CTCTGCGGCAAGTTTTTGGCAATGACTTGGGTATATTCTTACGTATCGGAAAGACTCAAGCACAGGAAGGA
590      600      610      620      630      640      650

700      710      720      730      740      750      760
AAACAGCCAAACAAACACTAATGAGTTTTTGAATTGATGTGGATAAAGGAGAAACTACTGTTTCAGTGTTC
AAACAAACACTACACATACCAATGAATCTTGAATTGATGTGGAAAAGGGGTAAGCTACTGCTTCTTCGCAC
660      670      680      690      700      710      720      730

770      780      790      800      810      820      830
AAGCAGTGATTCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTA-TGGGCCAGGAG
AAGCCGTGATTTTCTCCAGGAAACTAACCACAAGAGCCAGAAAGCATCACCAGTGCCTGAGCAATG-G
740      750      760      770      780      790      800

840      850      860      870      880      890      900
AAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTTTGGTTCATCCTTGTATCATC
AAGAGTGTCTGGGAGAAACACTCATCATTGTGGGAGCAGTGGTCTTCTGGTCACTGTCTTATCATCCTG
810      820      830      840      850      860      870

910      920      930      940      950      960      970
CTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAAT
CTGACCATATCTCTGTGCAAGCGCAGAAAGAACAGAGCAGGACAGAAAGGA---AGAACACCCCGTCGCGC
880      890      900      910      920      930      940

980      X
GTTTCATAA
TTGGCATAGACGAGGAGGCTGACGCTGCTGACTGTCACTGCCACACGGCACTGTTA
950      960      970      980      990      1000

```

11. FURM-969863-FIG2.SEQ (1-987)

RN07619 Rattus norvegicus Sprague-Dawley tissue factor pro

ID RN07619 standard; RNA; ROD; 1683 BP.

XX  
AC U07619;

XX  
DT 25-MAR-1994 (Rel. 39, Created)  
DT 25-MAR-1994 (Rel. 39, Last updated, Version 1)

XX  
DE Rattus norvegicus Sprague-Dawley tissue factor protein mRNA,  
DE complete cds.

XX  
KW .

XX  
OS Rattus norvegicus (rat)  
OC Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
OC Theria; Eutheria; Rodentia; Myomorpha; Muridae; Murinae.

XX  
RN [1]  
RP 1-1683  
RA Rosenfield C., Guha A., Nemerson Y., Taubman M.B.;  
RT "Rat tissue factor: its protein sequence and clotting properties  
RT are divergent from that of the mouse";  
RL Unpublished.

XX  
RN [2]  
RP 1-1683  
RA Rosenfield C.;  
RT ;  
RL Submitted (09-MAR-1994) to the EMBL/GenBank/DBJ databases.  
RL Claire-Lise Rosenfield, Medicine, Mount Sinai School of Medicine,  
RL One Gustave L. Levy Place, New York, NY 10029, USA

XX  
CC NCBI oi: 464010

RRU07619 Rattus norvegicus Sprague-Dawley tissue factor pro

LOCUS RRU07619 1683 bp mRNA ROD 25-MAR-1994  
 DEFINITION Rattus norvegicus Sprague-Dawley tissue factor protein mRNA,  
 complete cds.  
 ACCESSION U07619  
 KEYWORDS .  
 SOURCE rat  
 ORGANISM Rattus norvegicus  
 Eucaryotae; Metazoa; Chordata; Vertebrata; Gnathostomata; Mammalia;  
 Eutheria; Rodentia; Myomorpha; Muridae; Rattus.  
 REFERENCE 1 (bases 1 to 1683)  
 AUTHORS Rosenfield,C., Guha,A., Nemerson,Y. and Taubman,M.B.  
 TITLE Rat tissue factor: its protein sequence and clotting properties are  
 divergent from that of the mouse  
 JOURNAL Unpublished  
 STANDARD full automatic  
 REFERENCE 2 (bases 1 to 1683)  
 AUTHORS Rosenfield,C.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-MAR-1994) Claire-Lise Rosenfield, Medicine, Mount  
 Sinai School of Medicine, One Gustave L. Levy Place, New York, NY  
 10029, USA  
 STANDARD full automatic  
 COMMENT NCBI gi: 464010  
 FEATURES  
 Location/Qualifiers  
 sig\_peptide 64..144  
 source 1..1683  
 /strain="Sprague-Dawley"  
 /organism="Rattus norvegicus"  
 /cell type="aortic smooth muscle"  
 CDS 64..951  
 /note="NCBI gi: 464011"  
 /product="tissue factor protein"  
 /codon start=1  
 /translation="MAIPMRPRLAALAPTFLGFLLLQVAVGAGTPPCKAFNLTWIST  
 DFKTILEWQPKPTNYTYTVQISDRSRNWKYKCTGTTDTECDLTDIEVKDVNWTYEARV  
 LSPVWRNSTHGKETLFGTHGEPPFTNARKFLPYRDTKIGQPVIGKYEQGGTKLKVTV  
 KDSFTLVKRNKGTFLTLRQVFGNDLGYILTyrKDSSTGRKNTNTHNEFLIDVEKGVSY  
 CFFAQAIVFSRKTNHKSPESITKCTEQWKSVLGETLIIVGAVVFLVTVFIILLTISLC  
 KRRKNRAGQKRKNTPSRLA"  
 BASE COUNT 473 a 379 c 379 g 452 t  
 ORIGIN

Initial Score = 321 Optimized Score = 555 Significance = 21.64  
 Residue Identity = 60% Matches = 600 Mismatches = 321  
 Gaps = 69 Conservative Substitutions = 0

```

      10      20      30      40      50      60      70
CTCGCACTCCCTCTGGCCGCGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
          CTCTGTAGCGTAGCCTCC---GCGCCTCTG-----CTGAAGCC
          X          10          20          30

      80      90      100     110     120     130     140
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCCTGCCCCGGGTCCCGCGCC-CCGAGACCGC
CCGGACCTCGCCAGCAGCCCTTGACATGGCTATCCC--CATG---CG---CCCGCGCTCCTAG-CGGC
      40      50      60      70      80      90

      150     160     170     180     190     200     210
CGTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCC--CAGGTGGCCGGCTTCAGGCA---CTACAAAT
CCTCGCGCCAC-CT--TCTCGGCT--TCCTTCTCCTTCAGGTGGCCGTTGGTGCAGGCACTCCTCCAGGG
      100     110     120     130     140     150     160

      220     230     240     250     260     270     280
ACTGTGGCAGCATATAATTAACTTGGAAATCAACTAATTTCAGACAATTTTGGAGTGGGAACCCAAACCC
AAAG-CGTTTAATTAACTTGGATATCAACTGATTCAAGACAATCTTGGAGTGGCAACCGAAACCCACCAA
      170     180     190     200     210     220     230

      290     300     310     320     330     340     350
GTCAATCAAGTCTACACTGTTCAAATA-AGCACTA-AGTCAGGAGATTGGAAAAGCAAAATGCTTTTACACAA
CTATACCTACACTGTTTCAATAAGCGATAGATCTAGAAACTGGA-AATACAAATGCA----CTGGAACCACA
      240     250     260     270     280     290     300

      360     370     380     390     400
CAGACACAGAGTG---TGACCTACCGA---CGA-GATTGTGAA--GGA--TGTGAAGCA--GACGTA-CT
GAACTGAGTGTGACCTACCGACGAGATTGTGAAGGATGTGAAGTGGACCTATGAAGCAAGGGTCTATCT
      310     320     330     340     350     360     370

      410     420     430     440     450     460     470
-TGCAACGCTCTCTCTACCCGACGCAATATGAGAGA-CCACCGGTTCTGCTGGGAG---CTCTCTGA

```

50 60 70 80 90 100  
 TCC-CCAGC---CCCACG-GGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCC  
 TCCTGTAGCGTAGCCAACGCGCGCGCTGAAGCCCCGAGACCTCGCCTCCAGCCCTTGGACATGGCGATCC  
 80 90 100 110 120 130 140  
 110 120 130 140 150 160 170 180  
 CTGCCTGGCCCGGGTCCCGCGCC-CCGAGACCGCGCTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCCGC  
 --TCGTG---CG---CCCGCGCCTCCTAG-CGGCTCTCGCGCCACG---TTTCTCGGCTGCCTCCTCCTC  
 150 160 170 180 190 200  
 190 200 210 220 230 240 250  
 CAGGTGGCCGCGCTTCAGGCACTACAATACTGTGGCAGCATATAATTTAACTTGGAAATCAACTAATTTC  
 CAGGTGACCGCGGGTGCAGGCATTCCAGAGAAAG-CGTTTAAATTTAACTTGGATATCAACTGATTCAAGAC  
 210 220 230 240 250 260 270  
 260 270 280 290 300 310 320  
 AAGACAATTTGGAGTGGGAACCCAAACCCGTCATCAAGTCTACACTGTTCAAATAA--GCACTA-AGTCA  
 AATTTTGGAGTGGCAACCCAAACCCCAACTATACCTACACTGTACAGAT-AAGTGATCGATCTAGAAACT  
 280 290 300 310 320 330 340  
 330 340 350 360 370 380  
 GGAGATTGGAAGCAATGCTTTTACACAACAGACACAGAGTGTGACCTCA-CCGA---CG---AGATTGT  
 GGAA--ACAAG-TGCTTCTCGACCAC-AGACACCGAGTGCGACCTCACAGACGAGATCGTGAAGGATGT  
 350 360 370 380 390 400 410  
 390 400 410 420 430 440  
 GA--AGG--ATGTGAAGCAGACGTACT---TG--GCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGAG  
 GACCTGGGCCTATGAAGCAAAGTCTCTCTGTCCACGGAGGAAC---CAGTTCATGG-AGACGGAGAC  
 420 430 440 450 460 470  
 450 460 470 480 490 500 510  
 CACC---GGTTC-TGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAAC  
 CAACTTGTGATTCATGGGAGGAGCGCCATTTACAAACGCCCAAGTTTTTACCTTACCGAGACACAAAC  
 480 490 500 510 520 530 540 550  
 520 530 540 550 560 570 580  
 CTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAGAAGTGAACGG  
 CTTGGACAGCCAGTAATTCAGCAGTTTGAACAAGATGGTAGAAAACCTGAACGTGGTTGTAAGAACTCACTT  
 560 570 580 590 600 610 620  
 590 600 610 620 630 640 650 660  
 ACTTTAGTCAGAAGGAACAACACTTTTCTAAGCCTCCGGGATGTTTTTGGCAAGGACTTAATTTATACACTT  
 ACATTAGTCAGAAAGATGGTACATTCCTCACCCTGCGGCAAGTCTTTGGCAAGGACTTGGGTATATAATT  
 630 640 650 660 670 680 690  
 670 680 690 700 710 720 730  
 TATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTTTTGATTGATGTG  
 ACTTATCGGAAAGGCTCAAGCACGGGAAAGAAAACAAACATTACAAACACCAATGAATTCTCGATTGATGTG  
 700 710 720 730 740 750 760  
 740 750 760 770 780 790 800  
 GATAAAGGAGAACTACTGTTTCAAGTGTCAAGCAGTGATTCCTCCCGAACAGTTAACCGGAAGAGTACA  
 GAAGAAGGAGTAAGCTACTGCTTTTTTGTACAAGCTATGATTTTCTCCAGGAAAACCTAACCAAAATAGCCCA  
 770 780 790 800 810 820 830  
 810 820 830 840 850 860 870  
 GACAGCCCGGTAGAGTGTATGGCCAGGAGAAAGGG--GAATT--CAG--AGAAATATTCTACATCATTGGA  
 GGAAG--CAGTACAGTG--TGACC--GAGCAATGGAAGAGTTTCTGGGAGAAACACTCATCTTGTGGGA  
 840 850 860 870 880 890 900  
 880 890 900 910 920 930 940  
 GCTGTGGTATTTGTGGTCATCATCCTTGTATCATCCTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGA  
 GCAGTGGTGCTCCTGGCCACCATCTTTATCATCCTCCTGTCCATATCTCTGTGCAAGCGCAGAAAGAACCGA  
 910 920 930 940 950 960 970  
 950 960 970 980 X  
 GTGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA  
 GCGGGACAGAAAGGGA---AGAACACCCCGTGGCGCTTGGCATAGAGGAAAGGCTGAAGCGCTAACGCTCAC  
 980 990 1000 1010 1020 1030 1040  
 ACTGCCTGCACGGCACTGTTGCG  
 1050 1060



```

570      580      590      600      610      620      630
GAATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTT
500      510      520      530      540      550      560      570
GAACGTGGTTGTAAGAACTCACTTACATTAGTCAGAAAGAAATGGTACATTCCTCACCCTGCGGCAAGTCTT

640      650      660      670      680      690      700
TGGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAAA
580      590      600      610      620      630      640
TGGCAAGGACTTGGGTTATATAATTACTTATCGGAAAGGCTCAAGCACGGGAAAGAAAACAAACATTACAAA

710      720      730      740      750      760      770
CACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAACTACTGTTTCAGTGTCAAGCAGTGATTCCCTC
650      660      670      680      690      700      710
CACCAATGAATTCCTGATTGATGTGGAAGAAGGAGTAAGCTACTGCTTTTTTGTACAAGCTATGATTTTCTC

780      790      800      810      820      830      840
CCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGG--GAATT--CA
720      730      740      750      760      770      780
CAGGAAACTTAACCAAAATAGCCAGGAAG--CAGTACAGTG--TGCACC--GAGCAATGGAAGAGTTTCCT

850      860      870      880      890      900      910
G--AGAAATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTATCATCCTGGCTATATC
790      800      810      820      830      840      850
GGGAGAAACACTCATCATTTGTGGGAGCAGTGGTGCTCTGGCCACCATCTTTATCATCCTCCTGTCCATATC

920      930      940      950      960      970      980      X
TCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTCATAA
860      870      880      890      900      910      920
TCTGTGCAAGCGCAGAAAGAACCGAGCGGGACAGAAAGGGA---AGAACACCCCGTGGCGCTGGCATAGAG

GAAAGCGTGAAGCGCTAACGCTCACACTGCCTGCACGGCACTGTTGCG
930      940      950      960

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# 9. FURM-969863-FIG2.SEQ (1-987)

```

MUSTF      Mouse tissue factor (mtf) mRNA, complete cds.

LOCUS      MUSTF      1821 bp ss-mRNA      ROD      15-DEC-1989
DEFINITION Mouse tissue factor (mtf) mRNA, complete cds.
ACCESSION  M26071
KEYWORDS   membrane-bound glycoprotein; tissue factor.
SOURCE      Mouse (strain BALB/c) fibroblast 3T3 cell line, cDNA to mRNA, and
            DNA (bp 1-41), clone 3CH 482.
ORGANISM    Mus musculus
            Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
            Eutheria; Rodentia; Myomorpha; Muridae; Murinae.
REFERENCE   1 (bases 1 to 1821)
AUTHORS     Hartzell,S., Ryder,K., Lanahan,A.A., Lau,L.F. and Nathans,D.
TITLE       A growth factor-responsive gene of murine BALB/c 3T3 cells encodes
            a protein homologous to human tissue factor
JOURNAL     Mol. Cell. Biol. 9, 2567-2573 (1989)
STANDARD    full automatic
COMMENT      Draft entry and computer-readable sequence for [1] kindly submitted
            by S.Hartzell, 12-JUL-1989.
            NCBI gi: 201924
FEATURES
  mRNA      Location/Qualifiers
            29..1821
            /note="TFP mRNA"
  CDS       135..1019
            /note="tissue factor protein; NCBI gi: 201925."
            /codon start=1
            /translation="MAILVRPRLAALAPTFLGCLLLQVTAGAGIPEKAFNLTWISTD
            FKTILEHQPKNYTYTVQISDRSRNWNKCFSTTDECDLTDEIVKDVWYAEAKVL
            SVPRRNSVHGDGDQLVHGEPPFTNAPKFLPYRDTNLGQPVIGQFEQDGRKLNVVVK
            DSLTLVRKNGFTLRLQVFGKDLGYIITYRKGSSGTGKKNITNTNEFSIDVEEGVSYC
            FFVQAMIFSRKTNQNSPGSSTVCTEQWKSFLGETLIIVGAVVLLATIFIILLSISLCK
            RRKNRAGGKGKNTPSRLA"
  source    1..1821
            /organism="Mus musculus"
BASE COUNT  516 a      415 c      412 g      478 t
ORIGIN      Unreported

Initial Score      =      343      Optimized Score      =      582      Significance      = 23.29
Residue Identity   =      61%      Matches              =      632      Mismatches      =      321
Gaps               =      77      Conservative Substitutions      =      0

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X      10      20      30      40
CTCGCA--CTCCCTCTGGCCGG--CCCAGGGCGC-CTTCAGCCCAAC-C
TTTATAACGCACCCCGCGGACCCCGGCAGCCTGGGTACAGCCGGTACCCATCACTCGCTCCCTCCGATCGC
10      20      30      40      50      60      70

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## 8. FURM-969863-FIG2.SEQ (1-987)

MUSTFA Mouse tissue factor mRNA, complete cds.

LOCUS MUSTFA 1262 bp ss-mRNA ROD 23-JAN-1991  
DEFINITION Mouse tissue factor mRNA, complete cds.  
ACCESSION M57896 J05713  
KEYWORDS tissue factor.  
SOURCE Mouse (strain AKR) embryo fibroblast, cDNA to mRNA, clone c70.  
ORGANISM Mus musculus  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
Eutheria; Rodentia; Myomorpha; Muridae; Murinae.  
REFERENCE 1 (bases 1 to 1262)  
AUTHORS Ranganathan,G., Blatti,S.P., Subramanian,M., Fass,D.N., Maihle,N.J.  
and Getz,M.J.  
TITLE Cloning of murine tissue factor and regulation of gene expression  
by transforming growth factor type beta-1  
J. Biol. Chem. 266, 496-501 (1991)  
JOURNAL full automatic  
STANDARD NCBI gi: 201926  
COMMENT  
FEATURES  
CDS  
Location/Qualifiers  
35..919  
/note="NCBI gi: 201927"  
/product="tissue factor"  
/codon start=1  
/translation="MAILVRPRLAALAPTFLGCLLLQVIAGAGIPEKAFNLTWISTD  
FKTILENQPKPTNYTYTVQISDRSRNWKNCFSITDTECDLTDEIVKDVTHWAYEAKVL  
SVPRRNSVHGDDQLVIHGEPPFTNAPKFLPYRDTNLGQPVIIQFEQDGRKLNVVVK  
DSLTLVRKNGTFLTLRQVFGKDLGYIITYRKGSSGTGKKTNITNTEFSIDVEEGVSYC  
FFVQAMIFSRKTNQNSPGSSVCTEQWKSFLGETLIIVGAVLLATIFIILLSISLCK  
RRKNRAGQKGNTPSRLA"  
source  
1..1262  
/organism="Mus musculus"  
BASE COUNT 358 a 317 c 305 g 282 t  
ORIGIN  
Initial Score = 344 Optimized Score = 549 Significance = 23.36  
Residue Identity = 62% Matches = 593 Mismatches = 292  
Gaps = 71 Conservative Substitutions = 0

```

      20      30      40      50      60      70      80
GCCGGCCAGGGCGCCTTCAGCCCAACCTCCCAGCCCCACGGGCGCCACGGAACCCGCTCGATCTCGCCGC
                                     TGAAGCCCCGAGACCTCGCCTC
                                     X      10      20

      90     100     110     120     130     140     150
CAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCC-CCGAGACCGCGCTCGCTCGGACGCT
CAGCCCTTGGACATGGCGATCC--TCGTG---CG---CCCGCGCCTCCTAG-CGGCTCTCGCGCCACG--
      30      40      50      60      70      80

    160     170     180     190     200     210     220     230
CCTGCTCGGCTGGGTCTTCGCCCAGGTGGCGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTT
-TTCTCGGCTGCCTCCTCCTCAGGTGATCGCGGTGCAGGCATTCCAGAGAAAC-CGTTTAATTTAACTT
      90     100     110     120     130     140     150

    240     250     260     270     280     290
AACTTGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAAC--CCGTCAAT--CAAGTCTACA
GGATATCAACTGATTCAAGACA----ATTTGGAGTGGCAACCCAAACCCACCAACTATACCTACACTGTA
      160     170     180     190     200     210     220

    300     310     320     330     340     350     360
CTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCA--AATGCTTTTACACAACAGACACAGAGTGTGA
CAGAT-AAGTGATC---GATCTAGAACTGGAAGAAACAAGTGCTTCTCGACCAC-AGACACCGAGTGCGACC
      230     240     250     260     270     280

    370     380     390     400     410     420
CCTCA-CCGA---CG---AGATTGTGA--AGG--ATGTGAAGCAGACGTACT---TG--GCACGGGTCTTCT
TCACAGACGAGATCGTGAAGGATGTGACCTGGGCCTATGAAGCAAAGGTCTCTGTCCACGGAGGAACT
      290     300     310     320     330     340     350

    430     440     450     460     470     480     490
CCTACCCGGCAGGGAATGTGGAGAGCACC---GGTTC-TGCTGGGAGCCTCTGTATGAGAACTCCCAGA
CAGTTATG--GGGA---CGGAGACCAACTTGTGATTCATGGGAGGAGCCGCAATTTACAAACGCCCCAAA
      360     370     380     390     400     410     420

    500     510     520     530     540     550     560
GTTACACCTTACCTGGAGACAAACCTCGGACAGCCAACAATTCAGAGTTTTGAACAGGTGGGAACAAAAGT
GTTTTTACCTTACCGAGACACAAACCTCGGACAGCCAGTAATTCAGCAGTTTGAACAAGATGGTAGAAAAC
      430     440     450     460     470     480     490
```

CAGGGCGCCTTCAGCCCAACCTCCCGAGCCCAAGGGCGCCACGGAAACCCGCTCGATCTCGCCGCCAACTGG  
 850 860 870 880 890 900 910  
 TAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGTCCGCTCGGACGCTCCTGCTCG  
 100 110 120 130 140 150 160  
 TAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCGAGACCGCGTCCGCTCGGACGCTCCTGCTCG  
 920 930 940 950 960 970 980  
 GCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGG-CACT-ACA-AATACTGTGGCAGCATATAATTTAACTT  
 170 180 190 200 210 220 230  
 GCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGTGAGTGGCACCAGCCCTGGAAGCCCGGGCGCGCC--  
 990 1000 1010 1020 1030 1040 1050  
 GGAAATCAACTAATTTCAAGACAATTTTGAGTGGGAAC--CAAACCC--GTCAATCAAGTCTACACTGTT  
 240 250 260 270 280 290 300  
 --ACACGCAGGAGGGAGGCGACAGTCTTGG-CTGGCAGCGGGCTCGCCCTGGTTCCCGGGGCGCCCATGTT  
 1060 1070 1080 1090 1100 1110 1120  
 CAAATAAGC-CTAAGTCAGGAGATTG-GAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGAC-CTC  
 310 320 330 340 350 360 370  
 GTCCCCCGCGCTACGGGACTCGGCTGCGCTCACCAGCCCGGCTTGA-ATGA--ACCGAGTCCGTGCGGC  
 1130 1140 1150 1160 1170 1180 1190  
 ACCGACGAGATTGTGAAGGATGTGAAGCAGACGTAATTGGCAGGGTCTTCTCCTACC-CGGCAGGGAAT--  
 380 390 400 410 420 430 440  
 GCCCGCGGGAGT-TGCAGGGAG-GGAGTTGGCGCCCGAGACCCCG--CTGCCCTTCCGCTGGAGAGTTTGT  
 1200 1210 1220 1230 1240 1250 1260  
 GTGGAGAGCACCG-GTTCTGCTGGGAGCCTCTG--TATGAGAACTCCCAGAGTTCACACCTTA--CCTGG  
 450 460 470 480 490 500  
 CTGCGGGTGTCCGAGTAAT--TGGACTGTTGTGCATAAGCGGACT---TTTAGCTCCGCTTTAACTCTGG  
 1270 1280 1290 1300 1310 1320 1330  
 AGACAAACCT---CGGACAG--CCAACAATTGAGAGTTTGAACAGGTGGGAACAAAGTGAATGTGACCGT  
 510 520 530 540 550 560 570  
 GGAAAGGGCTTCCAGTGAGTTGCGACCTTCAATATGATAGGACTTGTGCTGCGTCTGCACGTGTTGGCGT  
 1340 1350 1360 1370 1380 1390 1400  
 AGAAGATGAACGGA-----CTTTAGTCAGAAG-GAA-CAACACTT--TCCTAAGCCTCCGGGATGTTTT--  
 580 590 600 610 620 630  
 -GCAGAGGTTTGGATATTATCTTTTATTATGTGCATCTTCCCTTAATAAGAGCGTCCCTGGTCTTTTCC  
 1410 1420 1430 1440 1450 1460 1470  
 TGGCAAGGACTTAATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAA--CA  
 640 650 660 670 680 690 700  
 TGGCCA--TCTT-TGTTCTAGGTTTGGGTAGAGGCAATCCAAAAGGGCTGGATTG----CTGCTTAGATTGG  
 1480 1490 1500 1510 1520 1530  
 AACACTAATGAGTTTTTGTATGATGGATAAAGGAGAAACTACTGTTTCAGTGTTCAGCAGTGATTCCC  
 710 720 730 740 750 760 770  
 AGCAGGTACAACGTTGTGCATGCCCCGTATTTCTACGAGGTGTTT-GGGACGGCTAGAGACTGGGA---CC  
 1540 1550 1560 1570 1580 1590 1600  
 TCCCGAACAGTTAACCGGAGAGTACAGACAGCC---CGGTAGAGTGATGGGCCAGGAGAAAGGGGAATTC  
 780 790 800 810 820 830 840  
 TGCTG---CGT--ACTGGCAAG--CAGACCTTCATAAGAAATAAT-CCTGATCCA--ATACAGCCGA---C  
 1610 1620 1630 1640 1650 1660  
 AGAGAAATATTCTACATCATTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTATCATCCTGGCTATATCT  
 850 860 870 880 890 900 910  
 GGTGTGACAGGCCACA-CGTCCCCG-TG-GGTCTCTGTGG-----AAGTTT-----CAGTGTAGCGACATTT  
 1670 1680 1690 1700 1710 1720  
 C-TACACAAGTGTAGAAAGGCAGGAGTGG---GGCAGAGCTGGAAGGAG---AACTC---CCCAC-TG--  
 920 930 940 950 960 970  
 CAGATAAAAGTGGAAAAAGTGAAGTTTGGCTTTTTTCATTGTATGCAGTCCTAACCTTTGTACACGTTGTG  
 1730 1740 1750 1760 1770 1780 1790  
 980 X  
 ----AATGTTT---CATAA  
 GGATTATCTTTTTTCCATAACTTACTGAAAACCCCTTCTGGCGGGCTGAACCTGACTCTTCTGAGCTGA  
 1800 1810 1820 1830 1840 1850 1860

## 7. FURM-969863-FIG2.SEQ (1-987)

HUMTFPB Human tissue factor gene, complete cds.

LOCUS HUMTFPB 13865 bp ds-DNA PRI 15-JUN-1989  
 DEFINITION Human tissue factor gene, complete cds.  
 ACCESSION J02846  
 KEYWORDS Alu repeat; cell surface integral membrane protein;  
 cell surface receptor; tissue factor.  
 SOURCE Human DNA, clones lambda-TF[559,679,753,885,1377].  
 ORGANISM Homo sapiens  
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
 Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.  
 REFERENCE 1 (bases 1 to 13865)  
 AUTHORS Mackman,N., Morrissey,J.H., Fowler,B. and Edgington,T.S.  
 TITLE Complete sequence of the human tissue factor gene, a highly  
 regulated cellular receptor that initiates the coagulation protease  
 cascade  
 JOURNAL Biochemistry 28, 1755-1762 (1989)  
 STANDARD full automatic  
 COMMENT Draft entry and computer-readable sequence for [1] kindly provided  
 by J.H.Morrissey, 25-OCT-1988.  
 NCBI gi: 339505  
 FEATURES  
 Location/Qualifiers  
 exon 922..1021  
 /number=1  
 /note="tissue factor"  
 pri\_m\_transcript 799..13232  
 /note="TF mRNA and introns"  
 intron 1022..2189  
 /note="TF intron A"  
 exon 2190..2301  
 /number=2  
 intron 2302..6391  
 /note="TF intron B"  
 repeat\_region 6127..6241  
 /note="Alu repeat partial copy A"  
 exon 6392..6591  
 /number=3  
 intron 6592..9288  
 /note="TF intron C"  
 repeat\_region 8391..8677  
 /note="Alu repeat copy B"  
 exon 9289..9467  
 /number=4  
 intron 9468..10074  
 /note="TF intron D"  
 exon 10075..10234  
 /number=5  
 intron 10235..11954  
 /note="TF intron E"  
 repeat\_region 10954..11249  
 /note="Alu repeat copy C"  
 exon 11955..12091  
 /number=6  
 repeat\_region 12458..12757  
 /note="Alu repeat copy D"  
 CDS join(922..1021,2190..2301,6392..6591,9289..9467,  
 10075..10234,11955..12091)  
 /gene="F3"  
 /note="tissue factor; NCBI gi: 339506."  
 /codon start=1  
 /translation="METPAWPRVPRPETAVARTLLLGVFAQVAGASGTTNTVAAYNL  
 TWKSTNFKTILEWPKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVQT  
 YLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTV  
 DERTLVRRNNTFLSLRDVFGKDLIYTLYYWSSSSGKKTAKTNTNEFLIDVDKGENYC  
 FSVQAVIPSRVTNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAI SLHK  
 CRKAGVGGSWKENSPLNVS"  
 source 1..13865  
 /organism="Homo sapiens"  
 BASE COUNT 3711 a 2955 c 3240 g 3959 t  
 ORIGIN 1 bp upstream of EcoRI site; chromosome 1.

Initial Score = 378 Optimized Score = 516 Significance = 25.91  
 Residue Identity = 56% Matches = 591 Mismatches = 340  
 Gaps = 119 Conservative Substitutions = 0

X 10 20

CTCGCACTCCCTCTGGCCGGCC

|||||

TATAGCGCGCGGGGACCGGCTCCCAAGACTGCGAGCTCCCGCACCCCTCGCACTCCCTCTGGCCGGCC

780 790 800 810 820 X 830 840

30 40 50 60 70 80 90

CGAGCTCCCAACAACTCTGGGCTCCCGCATCCCTCCCGTTTCATCCCGAGCCCA-GGTGCTCCAGCCC  
 10 20 30 X 40 50 60 70  
 40 50 60 70 80 90  
 AACCTCCC--CAGCCCCAC-----GGGCGCCACGGAACCCGCTCGATCTCGCCGCCAACTGGT  
 AACCTCGCAGCATCTCTACCTCTCCAGCCTCCGGGCTCAGCGGAATTTTGGAGCCTCGCCGTCAGCTCCG  
 80 90 100 110 120 130 140  
 100 110 120 130 140 150 160  
 AGACATGGAGACCCCTGCCTGGCCCGGGTCCCGGCCCCGAGACCGCGTCGCTCGGACGCTCCTGCTCGG  
 GGACATGGCGACCCCAACGGGCCCCGGGTGCCCTGCCCCAGGCGGAGTCGCTCGGGCTCTTCTATTTCGG  
 150 160 170 180 190 200 210  
 170 180 190 200 210 220 230  
 CTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACTTGGAA  
 CTTAGTCCTCATCCAGGGGCGCGGAGTCGCGGCACTACAGATGTAGTGGTAGCATATAATATAACTTGGAA  
 220 230 240 250 260 270 280  
 240 250 260 270 280 290 300 310  
 ATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCATCAAGTCTACACTGTTCAAATAAG  
 GTCAACTAATTTCAAGACCATTTTGGAGTGGGAACCCAAACCCATCAATCATGTCTACACTGTTCAAGATAAG  
 290 300 310 320 330 340 350  
 320 330 340 350 360 370 380  
 CACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAGAGTGTGACCTCACCAGCAGAT  
 CCCTAGATTAGGAACTGGAAAACAAATGCTTTTACACAACAAACAGGAGTGTGATGTCACTGATGAGAT  
 360 370 380 390 400 410 420 430  
 390 400 410 420 430 440 450  
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 TGTGAAAAATGTGAGAGAGACATATTTGGCAGAGTCTTCTCCTACCCCGCAGACACT-----ACCA---G  
 440 450 460 470 480 490  
 460 470 480 490 500 510 520  
 TTCTGCTGGGAGCCTCTGTATGAGAACTCCCCAGAGTTCACACCTTACCTGGAGACAAACCTCGGACAGCC  
 TTCCACAGTGGAGCCTCCGTTTACCAACTCCCCGAGTTCACACCTACCTAGAGACAAACCTTGGACAGCC  
 500 510 520 530 540 550 560  
 530 540 550 560 570 580 590  
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 570 580 590 600 610 620 630  
 600 610 620 630 640 650 660 670  
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 AGCGAACAGCGCATTCCTAAGCCTCCGGGATGTTTTGGCAAGGACTTGAATTACACACTTTATTACTGGAA  
 640 650 660 670 680 690 700 710  
 680 690 700 710 720 730 740  
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 720 730 740 750 760 770 780  
 750 760 770 780 790 800 810  
 AAACACTGTTTCAAGTTCAGGAGTATCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGT  
 AAACACTGTTTCAAGTTCAGGAGTATCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGCCCGGT  
 790 800 810 820 830 840 850  
 820 830 840 850 860 870 880  
 AGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTTGGAGCTGTGGTATTGTGGT  
 CAAGTGCCTAGCCACGAGAAAGTTCTGTCCACAGAACTTTCTTCATCATTTGGCACAGTGTGCTGGTGAT  
 860 870 880 890 900 910 920  
 890 900 910 920 930 940 950  
 CATCATCCTTGTCTATCCTGGCTATATCTTACACAAGTGTAGAAAGGAGGAGTGGGCGAGAGCTGGAA  
 CATCATCCTTGTCTATCCTGGCTATATCTTACACAAGTGTAGAAAGGAGGAGTGGGCGAGAGCTGGAA  
 930 940 950 960 970 980 990  
 960 970 980 X  
 GGAGAACTCCCACTGAATGTTTCATAA  
 GGAGAACACGCGCTCAACGCTGCATAAAAGATCCTGCTCTTGGAGCTTTCTGCCAACGCTGCAGAGCTCGT  
 1000 1010 1020 1030 1040 1050 1060 1070

CAGCCCAACAATTTCAGAGCTTTGAACAGGTGGGACAAAGTGAATGTGACCGTAGAAGATGAACGGACTTTA  
 450 460 470 480 490 500 510  
 600 610 620 630 640 650 660  
 GTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTAATTTATACACTTTATTAT  
 520 530 540 550 560 570 580  
 670 680 690 700 710 720 730  
 TGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAACTAATGAGTTTTTATTGATGATGGATAAA  
 590 600 610 620 630 640 650 660  
 740 750 760 770 780 790 800 810  
 GGAGAAAACACTACTGTTTCAAGTGTTCAGGAGTATCCCTCCCGAACAGTTAACCGGAAGAGTACAGACAGC  
 670 680 690 700 710 720 730  
 820 830 840 850 860 870 880  
 CCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATCATTGGAGCTGTGGTATTT  
 740 750 760 770 780 790 800  
 890 900 910 920 930 940 950  
 GTGGTCATCATCCTTG-TCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAGGCAGGAGTGGGGCAGAG  
 810 820 830 840 850 860 870  
 960 970 980 X  
 CTGGAAGGAGAACTCCCACTGAATGTTTCATAA  
 880 890 900 X 910 920 930 940  
 CGGGAAAGGAGAGCTCCCCCTGAACATCGCTGAAGGGAGCGCCGGGGCGGTGCCGGCTGCTGCCAATGCT  
 880 890 900 X 910 920 930 940  
 GTGTTGCACTGT  
 950

6. FURM-969863-FIG2.SEQ (1-987)

S74147 tissue factor [cattle, adrenal gland, mRNA, 1877 n

LOCUS S74147 1877 bp mRNA MAM 10-JUL-1992  
 DEFINITION tissue factor [cattle, adrenal gland, mRNA, 1877 nt]  
 ACCESSION S74147  
 KEYWORDS .  
 SOURCE cattle adrenal gland  
 ORGANISM Bos sp.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 1877)  
 AUTHORS Takayenoki,Y., Nuta,T., Miyata,T. and Iwanaga,S.  
 TITLE cDNA and amino acid sequences of bovine tissue factor  
 JOURNAL Biochem. Biophys. Res. Commun. 181, 1145-1150 (1991)  
 STANDARD full automatic  
 COMMENT GenBank staff at the National Library of Medicine created this  
 entry [NCBI gibbsq 74147] from the original journal article.  
 This sequence comes from Fig.2.  
 NCBI gi: 241438  
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 CDS  
 Location/Qualifiers  
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 NCBI gi: 241439"  
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 YLARVLSYPADTSSSTVEPPFINSPEFTPYLETNLGQPTIQSFEQVGTGLNVTVQDAR  
 TLVRANS AFLSLRDVFGKDLNYTLYYWKASSTGKKKATNTNGFLIDVDKGENYCFHV  
 QAVILSRVRNQKSPESPIKCTSHEKVLSTELFFIIGTVMLVIIIFIVVLSVSLHKCRK  
 VRAERSGKENTPLNAA"  
 source  
 1..1877  
 /organism="Bos sp."  
 /note="cattle"  
 BASE COUNT 529 a 416 c 412 g 520 t  
 ORIGIN  
 Initial Score = 443 Optimized Score = 759 Significance = 30.78  
 Residue Identity = 76% Matches = 770 Mismatches = 207  
 Gaps = 26 Conservative Substitutions = 0

X 10 20 30  
 CTCGCACCTCCCTCTGGCCGGCCAGGGCGCCCTTCAGCCC

LOCUS RABRTF 1753 bp ss-mRNA MAM 08-MAY-1991  
 DEFINITION Rabbit tissue factor mRNA, complete cds.  
 ACCESSION M55390  
 KEYWORDS tissue factor.  
 SOURCE Rabbit (strain New Zealand white) heart, cDNA to mRNA, clone pRTF1.  
 ORGANISM Oryctolagus cuniculus  
 Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;  
 Eutheria; Lagomorpha; Leporidae.  
 REFERENCE 1 (bases 1 to 1753)  
 AUTHORS Andrews,B.S., Rehmulla,A., Fowler,B.J., Edgington,T.S. and  
 Mackman,N.  
 TITLE Conservation of tissue fator primary sequence among three mammalian  
 species  
 JOURNAL Gene 98, 265-269 (1991)  
 STANDARD full automatic  
 COMMENT NCBI gi: 165696

FEATURES  
 mRNA  
 Location/Qualifiers  
 1..1753  
 /product="tissue factor"  
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 28..123  
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 mat\_peptide  
 124..903  
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 CDS  
 28..906  
 /note="NCBI gi: 165697"  
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 ARVLSYPARNGMTGFPPEPPFRNSPEFTPYLDTNLGOPTIGSFQVGTCLNVTQDA  
 RTLVRNGTFLSLRAVFGKDLNYTLYWRASSTGKKTATTNTNEFLIDVDKGENYCFS  
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 1..1753  
 /organism="Oryctolagus cuniculus"  
 BASE COUNT 455 a 394 c 471 g 433 t  
 ORIGIN

Initial Score = 560 Optimized Score = 693 Significance = 39.54  
 Residue Identity = 76% Matches = 702 Mismatches = 203  
 Gaps = 15 Conservative Substitutions = 0

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 ATCCGCAC-TCCTTGTGGGC--  
 X 10

100 110 120 130 140 150 160  
 CTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCGCTCGCTCGGACGCTCCTG  
 CT-TTGGACATGGCGCCCCCGACCCGGCTCCAGGTCCCGCGTCCCGGGACCGCTGTTCTTATACGGTGCTG  
 20 30 40 50 60 70 80 90

170 180 190 200 210 220 230  
 CTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTGGCAGCATATAATTTAACT  
 CTCGGCTGGTGTCTGCCAGGTGGCCGGCGCGCGAGACACTACAGGTA-----GAGCATATAATCTAACT  
 100 110 120 130 140 150

240 250 260 270 280 290 300  
 TGGAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCCGTCATCAAGTCTACACTGTTCAA  
 TGGAAGTCAACGAATTTCAAGACAATTTCTGGAGTGGGAACCCAAATCCATCGATCATGTCTACACAGTTACG  
 160 170 180 190 200 210 220

310 320 330 340 350 360 370  
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 ATAAGCACTAGGCTAGAAACTGGAAGAGCAATGTTTCTTAACCGCGGAGACGGAGTGGCAGCTACCGAT  
 230 240 250 260 270 280 290 300

380 390 400 410 420 430 440 450  
 GAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCGGCAGGGAATGTGGAGAGC  
 GAGGTGCTGAAGGACGTGGGGCAGACGTACATGGCGGGGTCTCTCCTACCCGGCAAGGAACGGAAACACC  
 310 320 330 340 350 360 370

460 470 480 490 500 510 520  
 ACCGGTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTACACCTTACCTGGAGACAAACCTCGGA  
 ACGGGTTCCTCCGAGGAGCCTCCCTTTAGAAACTCCCGGAGTTCAGCGCGTACCTGGACACAAACCTCGGC  
 380 390 400 410 420 430 440

530 540 550 560 570 580 590

exon /number=4  
490..650  
/number=5  
BASE COUNT 330 a 306 c 386 g 278 t  
ORIGIN

Initial Score = 561 Optimized Score = 608 Significance = 39.61  
Residue Identity = 77% Matches = 613 Mismatches = 169  
Gaps = 11 Conservative Substitutions = 0

```

150 160 170 180 190 X 200 210
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                                     GCAGACACTACAGGTA-----
                                     X      10

220 230 240 250 260 270 280
CAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTTGGAGTGGGAACCCAAACCGTCAATC
GAGCATATAATCTAACTTGAAGTCAACGAATTTCAAGACAATTTCTGGAGTGGGAACCCAAATCCATCGATC
 20 30 40 50 60 70 80

290 300 310 320 330 340 350 360
AAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAAAGCAAATGCTTTTACACAACAGACACAG
ATGCTCTACACAGTTCAGATAAGCACTAGGCTAGAAAAGTGAAGAGCAAATGTTCTTAACCGCGGAGACGG
 90 100 110 120 130 140 150 160

370 380 390 400 410 420 430
AGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTAAGTGGCACGGGTCTTCTCTACCCGG
AGTCCGACCTCACCGATGAGTCTGTGAAGGACGTGGGGCAGACGTACATGGCGCGGTCTCTCTACCCGG
 170 180 190 200 210 220 230

440 450 460 470 480 490 500
CAGGGAATGTGGAGAGCACCGGTTCTGCTGGGAGCCTCTGTATGAGAACTCCCAGAGTTCACACCTTACC
CAAGGAACGGAAACACCACGGGTTCCCGCAGGAGCCTCCCTTTAGAAACTCCCGGAGTTCACGCCGTACC
 240 250 260 270 280 290 300

510 520 530 540 550 560 570
TGGAGACAAACCTCGGACAGCCAACAATTAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTAG
TGGACACAAACCTCGGACAGCCAACAATTAGAGTTTTGAACAAGTGGGACAAACTGAATGTGACAGTCC
 310 320 330 340 350 360 370

580 590 600 610 620 630 640
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AGGATGCACGCACGCTGGTCAGAAGGAATGGGACATTCCTAAGTCTCCGGGCTGTGTTTGGCAAGGACTGA
 380 390 400 410 420 430 440

650 660 670 680 690 700 710 720
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ATTACACGCTTTATTACTGAGAGCTTCGAGCACAGGAAAGAAAACAGCCACGACAAACACTAATGAGTTTT
 450 460 470 480 490 500 510 520

730 740 750 760 770 780 790
TGATTGATGTGGATAAAGGAGAAAAGTACTGTTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAACC
TGATCGACGTGGATAAAGGAGAAAAGTACTGTTTTCAGTGTTCAGCAGTGATTCCCTCTCGGAAAAGGAAGC
 530 540 550 560 570 580 590

800 810 820 830 840 850 860
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AGAGAGCCCGGAGAGCCTCACTGAGTGCACAGCCGCGAGCAGGGCAGGGCCAGGGAGATGTTCTTCATCA
 600 610 620 630 640 650 660

870 880 890 900 910 920 930
TTGGAGCTGTGGTATTTGTGGTCATCATCCTTG-TCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAG
TTGGAGCAGTGGTGGTCTGTGGCCCT-----CTTGATCATCTGCTGTCTGTGACCGTGTACAAGTGCAGAAAG
 670 680 690 700 710 720 730

940 950 960 970 980 X
GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTCATAA
GCGAGGGCGGGGCCAGCGGGAAGGAGAGTCCCCCTGAACATCGCCTGAAGGGAGCGCGCGGGGGGTGC
 740 750 760 770 780 X 790 800

CGGCTGCTGCCAATGCTGTGTGCACTGT
 810 820 830
```



440 450 460 470 480 490 500  
 GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTACACCTTAC  
 GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGGAGCCTCTGTATGAGAACTCCCCAGAGTTACACCTTAC  
 410 420 430 440 450 460 470 480  
 510 520 530 540 550 560 570  
 CTGGAGACAAACCTCGGACAGCCAAACATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA  
 CTGGAGACAAACCTCGGACAGCCAAACATTCAGAGTTTTGAACAGGTGGGAACAAAAGTGAATGTGACCGTA  
 490 500 510 520 530 540 550  
 580 590 600 610 620 630 640  
 GAAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA  
 GAAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA  
 560 570 580 590 600 610 620  
 650 660 670 680 690 700 710 720  
 ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT  
 ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAAACAACTAATGAGTTT  
 630 640 650 660 670 680 690  
 730 740 750 760 770 780 790  
 TTGATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAAC  
 TTGATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAAC  
 700 710 720 730 740 750 760  
 800 810 820 830 840 850 860  
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 CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC  
 770 780 790 800 810 820 830 840  
 870 880 890 900 910 920 930  
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 ATTGGAGCTGTGGTATTTGTGGTCAATCCTTGTGTCATCATCCTGGCTATATCTCTACACAAGTGTAGAAAG  
 850 860 870 880 890 900 910  
 940 950 960 970 980 X  
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA  
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCACTGTTGGAGCTAC  
 920 930 940 950 960 X 970 980  
 TGCAAATGCTATATTGCACTGTGACCGAG  
 990 1000 1010

#### 4. FURM-969863-FIG2.SEQ (1-987)

OCBTF O.cuniculus mRNA for brain tissue factor  
 LOCUS OCBTF 1300 bp RNA MAM 31-OCT-1991  
 DEFINITION O.cuniculus mRNA for brain tissue factor  
 ACCESSION X53521  
 KEYWORDS brain tissue factor.  
 SOURCE rabbit  
 ORGANISM *Oryctolagus cuniculus*  
 Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;  
 Theria; Eutheria; Lagomorpha; Leporidae.  
 REFERENCE 1 (bases 1 to 1300)  
 AUTHORS Pawashe, A.B.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JUL-1990) Pawashe A.B., Yale University, SHM C 115,  
 Dept. of Molecular Biophysics & Biochemistry, 333 Cedar Street, POB  
 3333, New Haven, CT 06510, USA.  
 STANDARD full automatic  
 REFERENCE 2 (bases 1 to 1300)  
 AUTHORS Pawashe, A.B., Konigsberg, W.K. and Ezekowitz, M.D.  
 TITLE Molecular Cloning, Characterization and Expression of cDNA for  
 Rabbit Brain Tissue Factor  
 JOURNAL Thromb. Haemost. 66, 315-320 (1991)  
 STANDARD full automatic  
 COMMENT NCBI gi: 1495  
 FEATURES  
 source 1..1300  
 /organism="Oryctolagus cuniculus"  
 /strain="new zealand white rabbit"  
 exon <1..4  
 /number=1  
 exon 5..111  
 /number=2  
 exon 112..311  
 /number=3  
 exon 712..809

## 3. FURM-969863-FIG2.SEQ (1-987)

HUMTFPA Human tissue factor mRNA, complete cds, with an Al

LOCUS HUMTFPA 2104 bp ss-mRNA PRI 30-SEP-1988

DEFINITION Human tissue factor mRNA, complete cds, with an Alu repeat in the 3' untranslated region.

ACCESSION M16553

KEYWORDS Alu repeat; plasma membrane glycoprotein; tissue factor.

SOURCE Human placenta, cDNA to mRNA, clones lambda-hTF[3,7,8,12].

ORGANISM Homo sapiens  
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

REFERENCE 1 (bases 1 to 2104)

AUTHORS Scarpati, E.M., Wen, D., Broze, G.J. Jr., Miletich, J.P., Flandermeyer, R.R., Siegel, N.R. and Sadler, J.E.

TITLE Human tissue factor: cDNA sequence and chromosome localization of the gene

JOURNAL Biochemistry 26, 5234-5238 (1987)

STANDARD full automatic

COMMENT Draft entry and computer-readable sequence for [1] kindly provided by E.M. Scarpati, 04-AUG-1987.

NCBI gi: 339503

FEATURES

mRNA Location/Qualifiers  
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mat\_peptide 175..960  
/codon\_start=1  
/note="tissue factor"

repeat\_region 1330..1628  
/note="Alu repeat"

CDS 76..963  
/gene="F3"  
/note="tissue factor precursor; NCBI gi: 339504."  
/codon\_start=1  
/translation="METPAWPRVPRPETAVARTLLLGWVFAQVAGASGTTNTVAAYNL TWKSTNFKTILEWEKPVNQVYTVQISTKSGDWKSKCFYTTDTECDLTDEIVKDVKGTYLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFQVGTQVNVTVEDERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGENYCFVQAVIPSRVNRKSTDSPVECMGQEGFEIFYIIGAVAFVVIILVILAIISLHK CRKAGVGQSWKENSPLNVS"

source 1..2104  
/organism="Homo sapiens"

BASE COUNT 602 a 437 c 469 g 596 t

ORIGIN SmaI site; chromosome 1.

Initial Score = 958 Optimized Score = 961 Significance = 69.34

Residue Identity = 99% Matches = 961 Mismatches = 2

Gaps = 0 Conservative Substitutions = 0

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      X
      GGGTGCCTTCAGCCCAACCTCCCCAGCCCCACGGGCGCCACGGAACCC
      X      10      20      30      40

      80      90      100     110     120     130     140
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      |||
GCTCGATCTCGCCGCCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC
      |||
      50      60      70      80      90      100     110     120

      150     160     170     180     190     200     210
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
      |||
GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG
      |||
      130     140     150     160     170     180     190

      220     230     240     250     260     270     280
GCAGCATATAATTTAACTTGGAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
      |||
GCAGCATATAATTTAACTTGGAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCGTCAAT
      |||
      200     210     220     230     240     250     260

      290     300     310     320     330     340     350     360
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACA
      |||
CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTACACAACAGACACA
      |||
      270     280     290     300     310     320     330

      370     380     390     400     410     420     430
GAGTGTGACCTCACCACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCG
      |||
GAGTGTGACCTCACCACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCACGGGTCTTCTCCTACCCG
      |||
      340     350     360     370     380     390     400

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X 10 20 30 40 50 60 70  
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 X 10 20 30 40 50 60 70  
 80 90 100 110 120 130 140  
 GCTCGATCTCGCCGCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC  
 GCTCGATCTCGCCGCAACTGGTAGACATGGAGACCCCTGCCTGGCCCCGGGTCCCGCGCCCCGAGACCGCC  
 80 90 100 110 120 130 140  
 150 160 170 180 190 200 210  
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 GTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCAGGTGGCCGGCGCTTCAGGCACTACAAATACTGTG  
 150 160 170 180 190 200 210  
 220 230 240 250 260 270 280  
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 GCAGCATATAATTTAACTTGGAAATCAACTAATTTCAAGACAATTTGGAGTGGGAACCCAAACCCGTCAT  
 220 230 240 250 260 270 280  
 290 300 310 320 330 340 350 360  
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 CAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAATGCTTTTACACAACAGACACA  
 290 300 310 320 330 340 350 360  
 370 380 390 400 410 420 430  
 GAGTGTGACCTACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCCTACCCG  
 GAGTGTGACCTACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTCTTCTCCTACCCG  
 370 380 390 400 410 420 430  
 440 450 460 470 480 490 500  
 GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGAGCCTCTGTATGAGAACTCCCAGAGTTACACCTTAC  
 GCAGGGAATGTGGAGAGCACCGGTTCTGCTGGGAGCCTCTGTATGAGAACTCCCAGAGTTACACCTTAC  
 440 450 460 470 480 490 500  
 510 520 530 540 550 560 570  
 CTGGAGACAAACCTCGGACAGCCAAATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTA  
 CTGGAGACAAACCTCGGACAGCCAAATTCAGAGTTTTGAACAGGTGGGAACAAAGTGAATGTGACCGTA  
 510 520 530 540 550 560 570  
 580 590 600 610 620 630 640  
 GAAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA  
 GAAGATGAACGGACTTTAGTCAGAAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTGGCAAGGACTTA  
 580 590 600 610 620 630 640  
 650 660 670 680 690 700 710 720  
 ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAACACTAATGAGTTT  
 ATTTATACACTTTATTATTGGAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAACACTAATGAGTTT  
 650 660 670 680 690 700 710 720  
 730 740 750 760 770 780 790  
 TTGATTGATGTGGATAAAGGAGAAAACACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAAC  
 TTGATTGATGTGGATAAAGGAGAAAACACTGTTTCAGTGTTCAGCAGTGATTCCCTCCCGAACAGTTAAC  
 730 740 750 760 770 780 790  
 800 810 820 830 840 850 860  
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 CGGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAAATATTCTACATC  
 800 810 820 830 840 850 860  
 870 880 890 900 910 920 930  
 ATTGAGCTGTGGTATTTGTGGTCAATCCTTGTGTCATCCTGGCTATATCTCTACACAAGTGTAGAAAG  
 ATTGAGCTGTGGTATTTGTGGTCAATCCTTGTGTCATCCTGGCTATATCTCTACACAAGTGTAGAAAG  
 870 880 890 900 910 920 930  
 940 950 960 970 980 X  
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAA  
 GCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCACTGAATGTTTCATAAAGGAAGCACTGTTGGAGCTAC  
 940 950 960 970 980 990 1000  
 TGCAATGCTATATTGCACTGTGACCGAG  
 1010 1020 1030

```

640      650      660      670      680      690      700      710      720
GGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAAC
GGCAAGGACTTAATTTATACACTTTATTATTGGAAATCTTCAAGTTCAGGAAAGAAAACAGCCAAACAAAC
650      660      670      680      690      700      710      720

710      720      730      740      750      760      770      780
ACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGGAGTATTCCCTCC
ACTAATGAGTTTTTGTATTGATGTGGATAAAGGAGAAAACACTACTGTTTCAGTGTTCAGGAGTATTCCCTCC
730      740      750      760      770      780      790

790      800      810      820      830      840      850
CGAACAGTTAACCGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
CGAACAGTTAACCGAAGAGTACAGACAGCCCGGTAGAGTGTATGGGCCAGGAGAAAGGGGAATTCAGAGAA
800      810      820      830      840      850      860

860      870      880      890      900      910      920
ATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATCTCTACAC
ATATTCTACATCATTTGGAGCTGTGGTATTTGTGGTCATCATCCTTGTTCATCATCCTGGCTATATCTCTACAC
870      880      890      900      910      920      930

930      940      950      960      970      980      X
AAGGTGAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTCATAA
AAGGTGAGAAAGGCAGGAGTGGGGCAGAGCTGGAAGGAGAACTCCCCACTGAATGTTTCATAAAGGAAGCAC
940      950      960      970      980      990      1000

TGTTGGAGCTACTGCAAATGCTATATTGCACTGTGACCGAG
1010      1020      1030      1040

```

## 2. FURM-969863-FIG2.SEQ (1-987)

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HUMTFPC      Human tissue factor gene, complete cds, with a Alu

LOCUS      HUMTFPC      2127 bp ss-mRNA      PRI      15-DEC-1989
DEFINITION      Human tissue factor gene, complete cds, with a Alu repetitive
sequence in the 3' untranslated region.
ACCESSION      M27436
KEYWORDS      Alu repeat; plasma membrane glycoprotein; tissue factor;
transmembrane protein.
SOURCE      Human adult adipose, cDNA to mRNA, clone lambda-TF14.
ORGANISM      Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE      1 (bases 1 to 2127)
AUTHORS      Fisher, K.L., Gorman, C.M., Vehar, G.A., O'Brien, D.P. and Lawn, R.M.
TITLE      Cloning and expression of human tissue factor cDNA
JOURNAL      Thromb. Res. 48, 89-99 (1987)
STANDARD      full automatic
COMMENT      Draft entry and computer-readable copy of sequence [1] kindly
submitted by K.L.Fisher, 30-AUG-1989.
NCBI gi: 339507

FEATURES
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    repeat_region      1354..1651
                     /note="Alu repeat"
    repeat_region      1652..1662
                     /note="direct repeat flanking Alu sequence"
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DERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGENYC
FSVQAVIPSRTVNRKSTDSPVECMGQEKGEFREIFYIIGAVVFVVIILVILAILSLHK
CRKAGVGQSWKENSPLNVS"
    source      1..2127
               /organism="Homo sapiens"

BASE COUNT      606 a      450 c      472 g      599 t
ORIGIN
Initial Score      =      987      Optimized Score      =      987      Significance      = 71.51
Residue Identity    = 100%      Matches      =      987      Mismatches      =      0
Gaps      =      0      Conservative Substitutions      =      0

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mat\_peptide 214..996  
/codon\_start=1  
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CDS 112..999  
/gene="F3"  
/note="tissue factor versions 1 and 2 precursor; NCBI gi:  
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/codon\_start=1  
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YLARVFSYPAGNVESTGSAGEPLYENSPEFTPYLETNLGQPTIQSFEQVGTKVNVTV  
DERTLVRRNNTFLSLRDVFGKDLIYTLYYWKSSSSGKKTAKTNTNEFLIDVDKGENYC  
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CRKAGVGQSWKENSPLNVS"  
source 1..2141  
/organism="Homo sapiens"  
BASE COUNT 607 a 454 c 478 g 602 t  
ORIGIN 87 bp upstream of TaqI site [Cell 50, 129-135 (1987)].

Initial Score = 987 Optimized Score = 987 Significance = 71.51  
Residue Identity = 100% Matches = 987 Mismatches = 0  
Gaps = 0 Conservative Substitutions = 0

10 20 30 40 50 60  
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CGGGCGAACCCCTCGCACTCCCTCTGGCCGGCCAGGGCGCCTTCAGCCCAACCTCCCCAGCCCCACGGGC  
10 X 20 30 40 50 60 70  
70 80 90 100 110 120 130  
GCCACGGAACCCGCTCGATCTCGCCGCAACTGGTAGACATGGAGACCCCTGCCTGGCCCGGGTCCCGCGC  
GCCACGGAACCCGCTCGATCTCGCCGCAACTGGTAGACATGGAGACCCCTGCCTGGCCCGGGTCCCGCGC  
80 90 100 110 120 130 140  
140 150 160 170 180 190 200  
CCCGAGACCGCGCTCGCTCGGACGCTCCTGCTCGGCTGGGTCTTCGCCCAGGTGGCCGGCGCTTCAGGCACT  
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150 160 170 180 190 200 210  
210 220 230 240 250 260 270  
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220 230 240 250 260 270 280  
280 290 300 310 320 330 340  
AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC  
AAACCGTCAATCAAGTCTACACTGTTCAAATAAGCACTAAGTCAGGAGATTGGAAGCAAAATGCTTTTAC  
290 300 310 320 330 340 350 360  
350 360 370 380 390 400 410 420  
ACAACAGACAGAGTGTGACCTCACCGACGAGATTGTGAAGGATGTGAAGCAGACGTACTTGGCAGGGTC  
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370 380 390 400 410 420 430  
430 440 450 460 470 480 490  
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440 450 460 470 480 490 500  
500 510 520 530 540 550 560  
TTCACACCTTACCTGGAGACAACTCTGGACAGCCAACAATTGAGAGTTTGAACAGGTGGGAACAAAAGTG  
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510 520 530 540 550 560 570  
570 580 590 600 610 620 630  
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT  
AATGTGACCGTAGAAGATGAACGGACTTTAGTCAGAAGGAACAACACTTTCTAAGCCTCCGGGATGTTTTT  
580 590 600 610 620 630 640

4. OCBTF	O.cuniculus mRNA for	1555	361	608	39.76	0
5. RABRTF	Rabbit tissue factor mRNA, co	1753	560	693	39.54	0
**** 30 standard deviations above mean ****						
6. S74147	tissue factor [cattle, adrena	1877	443	759	30.78	0
**** 25 standard deviations above mean ****						
7. HUMTFPB	Human tissue factor gene, com	13865	378	516	25.91	0
**** 23 standard deviations above mean ****						
8. MUSTFA	Mouse tissue factor mRNA, com	1262	344	549	23.36	0
9. MUSTF	Mouse tissue factor (mtf) mRN	1821	343	582	23.29	0
**** 21 standard deviations above mean ****						
10. RRU07619	Rattus norvegicus Sprague-Daw	1683	321	555	21.64	0
11. RNO7619	Rattus norvegicus Sprague-Daw	1683	321	555	21.64	0
**** 11 standard deviations above mean ****						
12. MTPFZ1A	M.thermoformicum complete p	11014	179	435	11.01	0
**** 8 standard deviations above mean ****						
13. PSEPAHAB	P. putida DNA for reductase,	5840	149	419	8.76	0
14. XXMU01	Bacteriophage Mu genome right	1110	142	228	8.24	0
15. CLNCYCA	Clam cyclin A mRNA, complete	2163	139	429	8.01	0
**** 7 standard deviations above mean ****						
16. S55744	T cell receptor variable gamm	446	130	197	7.34	0
17. DATCVG1	O.aries rearranged T-cell rec	604	130	235	7.34	0
18. RNSCI11	Rat mRNA for brain sodium cha	6822	126	407	7.04	0
**** 6 standard deviations above mean ****						
19. PIGRI	Pig ribonuclease inhibitor (R	1256	125	418	6.96	0
20. BGHMGCOA	B.germanica mRNA for HMG-CoA	3433	124	426	6.89	0
21. M24537	Figure 2. Sequence of the spo	3360	122	410	6.74	0
22. BOVCNPA	Bos taurus (clone pCAMPDE-40)	2287	121	261	6.66	0
23. BACPBPE	Bacillus subtilis penicillin-	2362	120	415	6.59	0
24. HUMUT1002	Human STS UT1002.	532	119	217	6.51	0
25. BTCRYB1	Bovine mRNA for beta-crystall	860	119	377	6.51	0
26. HSEF1AL9	Human DNA for elongation fact	1823	119	336	6.51	0
27. DROGGBCS	D.melanogaster (clones T-beta	4590	119	416	6.51	0
28. GOTGLDBE	Goat beta globin locus activa	10194	119	421	6.51	0
29. HSCOMT1	H.sapiens catechol O-methyltr	1844	116	419	6.29	0
30. AA2LEFT	adeno-associated virus 2 left	2116	116	284	6.29	0
31. MFAPDA4A	M.fascicularis gene for apoli	2858	116	425	6.29	0
32. AA2CG	Adeno-associated virus 2, com	4675	116	425	6.29	0
33. PFPPF248	P.falciplarum DNA for erythro	509	115	203	6.22	0
34. HSARYLA	Human DNA for arylsulphatase	3637	115	399	6.22	0
35. BACMSQB	B.thuringiensis insecticidal	3753	115	422	6.22	0
36. HUMFGFAA	Human fibroblast growth facto	3901	115	418	6.22	0
37. MACP53A	Rhesus monkey p53 mRNA sequen	2184	114	416	6.14	0
38. XLAEI11M	X.laevis AE-III mRNA for pept	3618	114	427	6.14	0
39. S67111	{variable DNA region EhVR1} [	1669	113	392	6.07	0
40. HSDAO	H.sapiens diamine oxidase gen	9903	113	417	6.07	0

# 1. FURM-969863-FIG2.SEQ (1-987)

HUMTFP Human placental tissue factor (two forms) mRNA, co

LOCUS HUMTFP 2141 bp ss-mRNA PRI 15-JUN-1988

DEFINITION Human placental tissue factor (two forms) mRNA, complete cds.

ACCESSION J02931 J02681

KEYWORDS membrane-bound glycoprotein; procoagulant protein; tissue factor.

SOURCE Human placenta, cDNA to mRNA, clones lambda-[10,3 and 10,4] [2]; fibroblast cell line WI38, cDNA to mRNA, library of J.Sorge, clones lambda-CTF[2,3,4,5,22,23].

ORGANISM Homo sapiens

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria; Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

REFERENCE 1 (bases 79 to 1061)

AUTHORS Morrissey,J.H., Fakhrai,H. and Edgington,T.S.

TITLE Molecular cloning of the cDNA for tissue factor, the cellular receptor for the initiation of the coagulation protease cascade

JOURNAL Cell 50, 129-135 (1987)

STANDARD full automatic

REFERENCE 2 (bases 1 to 2141)

AUTHORS Spicer,E.K., Horton,R., Bloem,L.J., Bach,R., Williams,K.R., Guha,A., Kraus,J., Nemerson,Y. and Konigsberg,W.H.

TITLE Isolation of cDNA clones coding for human tissue factor: Primary structure of the protein and cDNA

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 84, 5148-5152 (1987)

STANDARD full automatic

COMMENT Draft entry and computer-readable sequence for [2] kindly provided by E.K.Spicer, 03-JUN-1987; and for [1] by J.H.Morrissey, 11-MAY-1987.

Two forms of tissue factor (light and heavy) are thought to be produced by differential cleavage at the 3' end of the signal peptide. The two forms of tissue factor are two amino acids different in length at the amino terminal of the mature protein and are otherwise identical.

A potential polyadenylation signal is located at positions 2119-2124.

NCBI gi: 339501

FEATURES Location/Qualifiers